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Direct Submission
Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University School submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Tel:03-3351-2370, Fax:03-3351-2370)
Location/Qualifiers
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Shimizu,N.
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humanexons or transcripts, for detecting expression and oth
thereof
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                      GTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGCACCTGCCGG
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AUTHORS
TITLE
JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 3 AB006685 DEFINITION Focus TITLE 2 (bases 1 to 1463)
Shimizu,N.
Direct Submission
Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University Schof Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio.ac. Nagamine, K., Peterson, P., Scott, H.S., Kudoh, J., Minoshima, S., Heino, M., Krohn, K.J.E., Lalioti, M.D., Mullis, P.E., Antonarakis, S.E., Kawasaki, K., Asakawa, S., Ito, F. and Shimizu Positional cloning of the APECED gene
Nat. Genet. 17 (4), 393-398 (1997) Nat. Genet. 98061086 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens APECED mRNA 9398839 APECED; AIRE-3 AB006685.1 GI:2696622 AB006685 (sites) 1463 A for bp mI AIRE-3, mRNA linear , complete cds. Euteleostomi; PRI Shimizu, 13-DEC-1997

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/mol type="mRNA"
/isolate="Caucasian"
/db_xref="taxon:9606"
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Homo sapiens APECED mRNA £
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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stage="3-yr-old"
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JOURNAL
1 (bases 1 to 2245)
Yaspo,M. and Lehrach,H.
NUCLEIC ACID MOLECULE ENCODING A (POLY) PEPTIDE CO-SEGREGATING
MUTLATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS
ECTODERMAL DYSTROPHY (APECED)
Patent: WO 9918197-A 1 15-APR-1999;
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                                                                                      TGGGCCATCCAGAGCATGGCCCGTCCGGCCCCCTTCCCCTCCTGACCCCAGATGGCC
                                                                                                                                                                          Teggccatccagagcategcccgtccggccgcccttcccctcgaccccagategcc
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Location/Qualifiers
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/mol_type="unassigned DN
/db_xref="taxon:32644"
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Pred. No. 3.2e-189;
0; Mismatches 4;
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AUTHORS
TITLE
JOURNAL
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FEATURES
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AUTHORS
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Paloti,A., Peltonen,L., Lee,Y.S., Francis,F., Henni
Lehrach,H. and Yaspo,M.L.
Lehrach,H. and Yaspo,M.L.
An autoimmune disease, ApBCEBD, caused by mutations
featuring two PHD-type zinc finger domains
Nat. Genet. 17, 399-403 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-JUL-1997) Max Planck Institut Innestrasse 73, Berlin D-141.95, Germany revised by submitter 24-SEP-1997 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aaltonen, J., Bjrses, P., Perheentupa, J., Horelli-Kuitunen, Paloti, A., Peltonen, L., Lee, Y.S., Francis, F., Hennig, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Homo Sapiens mRNA for AIRE
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/clone_lib="lambda GT
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/clone_lib="lambda_GT:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/chromosome="21"
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|mol_type="mRNA"
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WRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTL
VYKHLEAPPSAAFLPGLDSSALHFLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA
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PALHRDDLESLLSEHTFDGILQWAIQSMARPAAPPPS"

Ś 유정 음 성 음 성 음 당 á 밁 δ 밁 밁 S g δ 몽 5 S 망 δ 吊 5 밁 δ 밁 δ 문 δ S Query Match Best Local S Matches 1026 1771 1651 1176 1056 1471 1411 1111 1891 1831 1356 1296 1711 1236 1591 1116 1531 1351 1291 1231 1171 1051 atch 66.3%; cal Similarity 99.6%; 1026; Conservative 996 936 876 816 756 696 636 576 991 516 CTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGC TGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATC CAGCTCTGTGTTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAACCCTGCCCCAC GCCGGCCGGCTGGGATCAAGAAGGGGGACAGCGCCACCTCTTGTCAGTGCTCGGCTGTAAA GCCGGCCGGCTGGGATCAAGAAGGGGGACAGCGCCACCTCTTGTCAGTGCTCGGCTGTAAA CTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCAG CTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCAG AGCCCCGCCCGGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCT CGCTGCAGATCCTGCTCAGGAGACGTGACCCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCC GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGCCTG GGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCC GGTGCGCGTTGCGGGGTGTGCGGAGATGGTACCGGACGTGCTGCTGCGCGCC TCCTCGGCCCTGCACCCCCTACTGTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCT TCCTCGGCCCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGGTCAGCAGAACCTGGCTCCT ACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGGCTGGAC AGGTCGGCGGGAGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACG CGGGCAGAGGAGCCCCGGGCCCCAGGAGCCCGTGGAGACCCCGCTCCCCCGGGGCTT CCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCC CCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCC TGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCTCCGGGAGAGC CGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCC GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGCCTG ACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGAC AGGTCGGCGGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCCTAGCCGGCATGGACACG AGCCCCGCCCGCCTGGCCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCT Score 1023.6; DB 9; Pred. No. 3.2e-189; 0; Mismatches 4; Indels Length 0; Gaps 1415 1650 1055 1475 1890 1830 1355 1770 1295 1710 1235 1175 1590 1115 1530 1470 1410 1350 1290 1230 1170 1110 1050 995 935 875 815 695 635 575 755

1950

γ	Db 1	γQ	Db 1	Q	Qy Jb	Qy da	Db	Qy		δ	Db 1	γQ	Db	γ	Query Ma Best Loc Matches	ORIGIN	80	JOURNAL	AUTHORS	ORGANISM	VERSION KEYWORDS	DEFINITION ACCESSION	RESULT 7 CQ731864 LOCUS	Db 2	0у 1	Db 1	Qy
996 GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGGCACGGGACGGGCCTG	418	936 GGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCC	i.s	876 TCCTCGGCCCTGCACCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGC	816 ACTCTTGTCTACAAGCACCTGCCGGCTCCCGCCTTCTGCAGCCCCGCCTGCCAGGTCTGGAC	756 AGGTCGGCGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAACCCGGCATGGACACG	8	696 CGGGCAGAGGAGCCCCGGCCCAGGAGCCACCCGTGGAGACCCCCGCCCCCCCC	1118 CCCAGTGGGACCTGGAGGTGCCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCAGCCC	636 CCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCA	0	576 TGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGA	998 CTCCACCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGGGGGGG	516 CTGTGCCAGAAGAATGAGGACGAGTGTGCGGTGTGTCGGGACGGCGGGGAGCTCAT	ery Match 66.3%; Score 1023.6; DB 6; Length 2258; st Local Similarity 99.6%; Pred. No. 3.2e-189; tches 1026; Conservative 0; Mismatches 4; Indels 0; G		ce 12258 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Patent: WO 02068579-A 17798 06-SEP-2002; PE Corporation (NY) (US) PE Corporation/Qualifiers	RS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and othe	4 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	CQ731864.1 GI:42309571 Homo ganjeng (himan)	Sequence 17798 from Patent WO02068579. CQ731864	CQ731864 2258 bp DNA linear PAT 03	 2011 AAATTAGCTG 2020	536	.951 TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAA	476 TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAAT
CCTG 1055	GCC 1477	36CC 99S		CCT 935	GAC 875	ACG 815 ACG 1297		3CTT 755	3CCC 1177	3CCC 695	ATC 1117	ATC 635	TGC 1057	TGC 575	aps 0;				of her uses	ostomi;			-FEB-2004			TAA 2010	TAA 1535

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                                                                                                                                 Direct Submission
Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (B-mail:shimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370(ex.2720),
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Shimizu, N.
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Nat. Genet. 17 (4), 393-398 (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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join(4580. .4838,5257. .5431,5678. .5833,6217. .6291,
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16355. .16688)
16355. .16688)
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                                                                                                                              TTGGTGTACAGTTCCGGGGCCCCCTGGAACGCAGCAGCCTGCAAGAAACCGGGTTTTCTTC
                                                                                                                                                                      AGGTCGGGAGAGACCTCCCTGGGCCTGGCCCCACTGCCCTGTGAGGAAGGGTTCATGTGG
CAGGGCAGAATTTCAGGCCCTGGCAGCATGGGAGCAGGGCAGAGACTGGGGAGTTCAGGT
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PLLCVGPEGQQNLAPGAAGEVCCDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCR
CCSGNYTPAPVEGVLAPSPARLAPGPAKDDTASHEPALHRDDLESLLSEHTFDGILQW
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QEPPVETPLPPGLRSAGEEPRCQGWTPRPCTPYCVWVLRVSRTWLLVRVAGCAEMVRT
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12489. .12610,13100. .13137)
/gene="APECED"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-JUL-1998) Steffen Hennig, MPIMG, Abt. Lehrach, Max
Planck Institut fuer Molekulare Genetik, Ihnestrasse 73, Berlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Lee, Y.S., Francis, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An autoimmune disease, APECED, caused by mutations in a novel featuring two PHD-type zinc finger domains
Nat. Genet. 17, 399-403 (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              /note="(GAAAA)n
                                            /note="Alusq/x"
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Location/Qualifiers
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AP001060
                                                                                                                         Submitted (12-JAN-2000) Nobuyoshi Shimizu, Keio University, Sof Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 42133)
Shimizu,N., Kudoh,J. and Shibuya,K.
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Shimizu,N. Kudoh,J. and Shibuya,K.
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                   Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauez, G., Bloceker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and Yaspo, M.L., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
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Homo sapiens genomic DNA, chromosome 21q,
AP001754 AL163299 BA000005
AP001754.1 GI:7768775
Submitted (10-ARR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)

On May 30, 2000 this sequence version replaced gi:7717429.

The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan,
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Nature 405 (6784), 311-319 (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* e.mail: nshimizu@dmb-med.keio.ac.jp/
* URL: http://www.dmb.med.keio.ac.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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                                                                                                                                                                                              /clone lib="KU21-D Cosmid library"
/note="Accession No. AP001063"
97304. .135091
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                                                        /chromosome="21"
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/note="Accession No. AP001061"
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GSVPAPLALPSDPQLHQNGEDEAVCRDGGELICCDGCGPAFHLACLSFPBLREIFSGQ
GSVPAPLALPSDPQLHQNGEDEAVCRDGGELICCDGCGTAFHLACLSFPBGEPLAGMDTTL
                                                                                                                                                                                                                                                                                                                                                                                                1508. 1627

/gene="AIRE"

join(1628. .1759,2178. .2352,2599. .2754,3138. .3212,

3966. .4079,5278. .5423,5609. .5689,6716. .6831,7923.

8614. .8796,9410. .9531,10022. .10124,12004. .12066,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="P314N7, 3' partial"
/clone lib="RPCI1,3-5 PAC library"
/note="Accession No. AJ011930"
1508. .13840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="KB1399C7, 3' partial"
/clone lib="Keio BAC library"
/note="Accession No. AP001067"
280806, .>340000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="AIRE"
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join(6508. 1759,5278. 5423,5609. 5689,6716. 6831,7923.
3966. 40799,5278. 5423,5609. 10124,12004. 12066,
8614. 8796,9410. 9531,10022. 10124,12004. 12066,
                                               PALHRDDLESLLSEHTFDGILQWAIQSMARPAAPFPS"
                                                                 VYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA
AAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVLAPSPARLAPGPAKDDTASHE
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                                                                                                                                                                                                                                                       /codon_start=1
/product="autoimmune regulator (APECED
/protein_id="BAA95560.1"
/db_xref="GI:7768776"
                                                                                                                                                                                                                                                                                                                                        13277. .13348)
/gene="AIRE"
/note="Accession No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="autoimmune regulator (APECED note="Accession No. Z97990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="AIRE"
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mol_type="genomic DNA"
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/note="Accession No. AP001065"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DN
/db_xref="taxon:9606"
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VERSION
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Best Local Sim
Matches 469;
                                                                                                                                                                                                                                                                                                                                                              CONSRTM
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes chromosome 22 clone CH251-479II3 map 22q22.3, complete sequence.
The Chimpanzee Chromosome 22 Sequencing Consortium cons
*Chinese National Human Genome Center at Shanghai,
Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany;
*Institute of Molecular Biotechnology, Jena, Germany;
*KRIBB Genome Research Center, Daejeon, Korea;
*MAX-Planck-Institute for Molecular Genetics, Berlin,
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center,
                                                                                                                                                                                                                               2 (bases 1 to 143192)
Kube, M., Sudbrak, R., Mueller, I.,
Heitmann, K., Gimmel, V., Beck, A.,
Yaspo, M.L. and Reinhardt, R.
                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 143192)
                                                                                                                                                                                             Submitted (18-DEC-2002)
                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                           The Chimpanzee Chromosome 22 Sequencing Consortium DNA sequence of chimpanzee chromosome 22 and its e
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                                                                                                                                                                                                                                                                                                                                          implications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCAGAGATGCTGCTGGGGGAGCTGTTTTTGGGAAGGAGGTTGCCTCTCAGGAGGGTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCCAGCCCAGTCTGCATGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGGCAGAATTTCAGGCCCTGGCAGCATGGGAGCAGGGCAGAGACTGGGGAGTTCAGGT
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2599. .2754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 462.4; DB 9;
Pred. No. 2.7e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                          Thiel, J., Klages, S., Borzym, K., Ben Kahla, A., Lehrach, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                       consists
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                                               Germany;
          Taipei
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6613 422 6553 6493 302 6433 242

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                                                                                                                                                                            ORIGIN
                                                                                      Query Match
Best Local Similarity
Matches 462; Conserv
                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                             183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/chimpanzee251.htm. The clone may be obtained from Pieter J. de Jong and coworkers (http://www.chori.org/bacpac). VECTOR: pTARBAC2.1
IMPORTANT: This sequence is not the entire insert of clone CH251-479II3 It may be shorter because we sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The CHORI-251 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al.Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assembly was confirmed by restriction digest. ----
Neighboring sequence information:
This clone is overlapped by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               characteristics are described at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taiwan;
*RIKEN Genomic Sciences Center, Yokohama, Japan.
AGGTCGGGAGAGACCTCCCTGGGCCTGGCCCCACTGCCCCTGTGAGGAAGGGTTCGTGTGG, 37969
                                        AGGTCGGGAGAGACCTCCCTGGGCCTGGCCCACTGCCCTGTGAGGAAGGGTTCATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: pUC18; 100% of reads chemistry: Dye-terminator Big Dye, 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 143190 bases at least Q40 Consensus quality: 143192 bases at least Q30 Consensus quality: 143192 bases at least Q30 Consensus quality: 143192 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CH251-479I13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Max-Planck-Institute for Molecular Genetics Center code: MPIMG_
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTB-061A04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage:
                                                                                                                                                                                                                                                                                                          141389.
                                                                                                                                                                                                                                                                                                                                                                                                                                         <1. .14090
                                                                                                                                                                                           'note="overlapping clone"
                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-061A04"
                                                                                                                                                                                                                                                                             organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                      note="overlapping clone"
|41389. .>143192
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CH251-479I13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="22q22.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   clone="PTB-051003"
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sections only once, except for a short overlap.
                                                                                                                                                                                                                                                                                                                                                                     xref="taxon:9598"
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                                                                                                        Score 451.2; DB 9
Pred. No. 4.7e-78;
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                                                                                                                                                                                                                                                                                                 3 (bases 1 to 1656)
Ruan,Q.G., Wang C.Y., Shi,J.D. and She,J.X.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1656)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y.Q.,
Detter,J.C., Davoodi-Sermiromi,A. and She,J.X.
Complete genomic sequence, gene structure and localizati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detter, J.C. and She, J.X.
Chromosomal localization and complete genomic sequence of the murine autoimmune regulator gene (Aire)
Autoimmunity 31 (1), 47-53 (1999)
                                                                                                                                                                                                                                                                             Submitted (17-FEB-1999) Pathology,
                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                       mouse Aire gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1656)
Shi, J.D., Wang, C.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                      /gene="Aire"
                                                               /map="between D10Mit31 and
1. .>1656
                                                                                                                            db_xref="taxon:10090"
                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                          chromosome="10"
                                                                                                                                                                       mol_type="mRNA"
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mRNA, partial ROD 26-OCT-2001

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                                        GCTGGCCCCAGCCCCGCCCGCCTGGCCCTGGGCCTGCCAA-----GGATGACACTGC
                                                                                                                                                                                          TCTCCGCTGCAAATCCTGCTGCAGACTCGACTCCCACGCCAGGCACACCGGGCGAAGC
                                                                                                                                                                                                                                       CCTGCGCTGCAGATCCTGCTCAGGAGACGTG-----ACCCCAGCCCCTGTGGAGGGGGGT 1105
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/product="autoimmune regulator"
/protein_id="AAP36481.1"
/protein_id="AAP36481.1"
/db_xref="dl:7108573"
/protein_id="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
/translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
/translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLHALAXGSVSSPGSHLK
COUTLAGEKGCPQAFHALLSWLLPREPTKRKALEEFRATPPATILAXGSVSSPGSHLK
TKPPKKPDGNLESQHLFUGNGIQTMAASVQRAVTVASGDVPGTRCAVEGILIQVYES
GRSKKCIQVGGBFYTPNKFEDPSGNLKNKARSGGSLKPVTVARKGAQVTIPGRDEQKVG
QQCGVPPLPSLDSEPQVQKNEDDECAVCBGLICCDGCPRAFHLACLSPPLQEIPS
GLWRCGCCLQGRVQQNLSQPEVSRPPELPAETPILVGLKSASEKTRGEBSELKASSDA
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AAFHWRCHFPTAAARFGTNLRCKSCSADSTFTPGTPGBBARCSVCGDGTEVLRCAHCA
AAFHWRCHFPTAAARFGTNLRCKSCSADSTFTPGTPGBBARCSVCGDGTEVLRCHCA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1656)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G.,
Detter,J.C., Davoodi-Sermiromi,A. and She,J.)
Complete genomic sequence, gene structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detter, J.C. and She, J.X.
Chromosomal localization and complete murine autoimmune regulator gene (Aire Autoimmunity 31 (1), 47-53 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruan, Q.G., Wang C.Y., Direct Submission
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G.,
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/product = "autoimmune regulator"
/protein id="AAF36482.1"
/protein id="AAF36482.1"
/db xref="GI:7108575"
/translation="WAGGGGWLRRELLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
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KDVDLNQSRKGRKPLAGFKAAVLPPFPFKRKALEEPRATPPATLASKSYGSPGSHLK
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GRSKKCIQVGGEFYTPNKFBDPSGNLKNKARSGSSLKFVVRAKGAQVTIPGRDEQKVG
QQCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEVGRPELPAETPILVGLRSASEKTRGPSRELKASSDA
AVTYVNLLAPHPAAPLLEPSALCPLLSAGNEGRPFAPSARCSVCBGTEVLRCHCA
AAFHRGCHFTAAARRGTNLRCKSCSADSTFTEGTPGEAVFTSGPRAPGLAKVGDDS
ASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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/mol_type="mRNA"
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/strain="NOD"
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Patent: WO 9918197-A 10 15-APR-1999;
MAX PLANCK GESELLSCHAFT (DE); YASPO MARIE LAURE (DE)
1. 1659
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                                    CGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCCCGTTCCGGCGGCCCCCTTCCCCTC
                                                                      TAGTCACGACCCTGTTCTACATAGGGACGACCTGGAGTCCCTCCAATGAGCACTCATT
                                                                                   TGTACCCACCTCTGGGCCCCGTCCAGCACCTGGGCTTGCCAAGGTAGGGGACGACTCTGC
                                                                                                                                                                 TCTCCGCTGCAAATCCTGCTCTGCAGACTCGACTCCCACGCCAGGCACACCGGGCGAAGC
                                                                                                                                                                              CCTGCGCTGCAGAATCCTGCTCAGGAGACGTG-----ACCCCAGCCCCTGTGGAGGGGGT
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ilarity 68.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
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Pred. No. 5.8e-65;
0; Mismatches 244
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Best Local S
Matches 580
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Mus musculus mRNA for Aire
AJ132243.1 GI:4456674
AJ132243.1 GI:e456674
Aire gene; Aire protein.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                              580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-JAN-1999) Karin B., Max Planck Institute for
Molecular Genetics, Ihnestrasse 73, Berlin D-14195, German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blechschmidt, K., Schweiger, M., Wertz, K., Poulson, R., Christensen, H.M., Rosenthal, A., Lehrach, H. and Yaspo The mouse Aire gene: comparative genomic sequencing, organization, and expression Genome Res. 9 (2), 158-166 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular Genetics, Ihnestrasse
Location/Qualifiers
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                           Similarity
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                CTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCCTGTCCCCTCCGGCA
                                                         CCAGGTTAACCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGAGGTGAGCTCAT
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                             /gene="Aire"
/codon_start=1
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GRSKKCIQVGGEFYTPNKFEDPSGNLKNKARSGSSLKPVVRAKGAQVTIPGRDEQKVG
QQCGVPPLPSLPSEPQVNQKNEDDECAVCHDGGELICCDGCFRAFHLACLSFPLQEIPS
GLWRCGCCLQGRVQNULSQPFVSRPPELPAETPILVGLRSASEKTRGPSBELKASSDA
AVTYVNILLAPHPAAPLLEFSALCFLLSAGNEGRPGPAFARCSVCGDGTEVLRCAHCA
AAFHWRCHFFTAAARFGTNLRCKSCSADSTFTPGTPGEAVPTSGRPAPGLAKVGDDS
ASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPFTSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
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/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="Aire"
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Pred. No. 5.8e-65;
0; Mismatches 244;
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    and Yaspo, M.L.
sequencing, gene

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Mus musculus mRNA for APECED pr
AJ243821.1 GI:6706792
Aire gene; APECED protein.
Mus musculus (house mouse)

Mus musculus

Mus musculus

Mus musculus; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
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                                                                        Kolmer, M.
                                                                                                  Unpublished
                                                                                                               Ulmanen, I. and Kolmer, M. Expression of the mouse
                                                                                                                                            Halonen, M., Pelto-Huikko, M.,
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                                                                                   (bases 1 to 1906)
Location/Qualifiers
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protein
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Direct Submission
Submitted (14-UTL-1999) Kolmer M., Department of Human Molecular
Generics, National Public Health Institute, Mannerheimintie 166,
Helsinki, FIN-00300, FINLAND
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Sciurognathi; Muridae;
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GETTLRLKEKEGCPQAFHALLSWLLTRUSGAILDFWRILFWNYLLERYSRLHSILDGFP
KDVDLNQSRKGRKPLAGPKAAVLPFRPTKRKALEEPRATPPATLASKSVSPGSSLK-
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGEEFYTPNKFEDPSGNLKNKARSGSSLKFVVRAKQAVTIPRDEQKVG
QQGVPPLPSLPSEPQVNQKNEDBCAVCHDGGELICCDGCPAKGAQVTIPPLQFDFQCTVF
QQCGVPPLPSLPSEPQVNQKNEDBCAVCHDGGELICCDGCPAKGAQVTIPPLQFLRSASDA
AVTYVULLAPHPAAPLLEPSALCPLASAGNEGRPGPABSARCSVCGDGTEVLRGAHCA
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/db_xref="GI:6706793"
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_xref="Swiss-Prot:Q9Z0E3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
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Ruan, Q.G., Wang, C.Y.,
Direct Submission
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Ruan,O.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the regulator gene (Aire)
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Mammalia; Eutheria; Rodentia;
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AF128116
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        /codon_start=1
/protain_t="autoimmune regulator"
/protain_id="Autoimmune regulator"
/protain_id="Autoimmune regulator"
/protain_id="Autoimmune regulator"
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/db_xref="GI:7108534"
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GRSKKCIQVGGEFYTPNKFEDPSGNLKMKARSGSSLKPVVRAKGAQGRDEQKVGQQCG
VPPLPSLPSEPQVNQKMEDECAVCHDGGELICCDGCPRAFHLACLSPPLGEIPSGLWR
CSCCLQGRVQONLSQDEVSRPPELPAETPILVGLRSASEKTRGPSRELKASSDAVTY
VNLLAPHPAAPLLEPSALCPLLSAGNEGRPEPAPGARCSVCGDGTEVLRCHCAAAFH
WRCHFPTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTTGGPRPAPGLAKVGDDSASHD
PVLHRDDLESLLNEHSFDGILQMAIQSMSRPLAETPPPSS"
                                                                                                                                                                                                                                                                                                                                                  /gene="Aire"
58. .1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/strain="B6"
                                                                                                                                                                                                                                                                                                       /function="transcription factor"
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Location/Qualifiers
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Query Match Best Local Similarity

25.0%;

Score 385.6; DB 10; Pred. No. 5.7e-65;

Length 1924;

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KEYWORDS
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Wang,C.Y., Shi,J.D., Davoodi-Semirom Direct Submission
Submitted (21-JUL-1998) Pathology, I. Medicine, University of Florida, 160
FL 32610, USA
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1 (bases 1 to 1936)

Wang,C.Y., Shi,J.D., Davoodi-Semiromi,A. and She,J.X.

Cloning of Aire, the mouse homologue of the autoimmune regulator

Cloning of Aire, the mouse homologue of the autoimmune typolyglandular syndrome typolyglandular syndr
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CACGACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGTTAACCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGACGGAGGTGAGCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGGCCCAGTCTGCATGGGCGTCTC
                                                                         ACTGAGGTCAGCTTCAGAGAAAACCAGGGGCCCATCCAGGGAGCTCAAAGCCAGCTCTGA
                                                                                                               GCTTAGGTCGGCGGGAGGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGA
                                                                                                                                                                       GTCCCAGCCTGAGGTGTCCAGGCCCCCGGAGCTACCTGCAGAGACCCCCGATCCTCGTGGG
                                                                                                                                                                                                   GCCCCGGGCAGAGGAGCCCCGGCCCCAGGAGGCCACCCGTGGAGACCCCGCTCCCCCCGGG
                                                                                                                                                                                                                                                                     GATCCCCAGTGGCCTCTGGAGATGCTCCTGCTGCCTCCAGGGCAGAGTCCAACAGAACCT
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OBTIRLIKEKEGCPQAFHALLSWLLTROSGAILDFWRILFKONTLERYSRLHSILDGFK
KOVDLNOGRKGRKFLAGPKAAVLPFRPPTKRKALEERPAFTPANTLASKSVSBOSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQOVFES
GRSKKCIQVGGEFYTPKKFEDPSGNLKNKARSGSSLKFVVRAKGAQVTIDGRDEQKVG
QQCGYPPLPSLPSEQVUQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEVSRPPELPAETPILVGLRSASEKTRGPSRELKASSDA
AVTYVNLLAPHPAPLLEPSALCPLLSAGNUGGREPAPSARCSVCGDGTEVLRCAHCA
AAFHNCHFFTTAAARPGTNLRCKSCSADSTFTPGTPGBASARCKYGDDGTEVLRCALGCA
AAFHNCHFFTTAAARPGTNLRCKSCSADSTFTPGTPGBAPGFRAFGLAKVGDDS
ASHDPVLHRDDLESLLNEHSFDGILQMAIQSMSRPLAETPPFSS"
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58. .1716
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/product="autoimmune regulator"
/protein_id="AAD20444.1"
/db_xref="GI:4426599"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain="B6"
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68.9%;
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Pred. No. 5.7e-65;
0; Mismatches 244;
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1600 SW Archer Road, Gainesville,
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                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; I Mammalla; Eucheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 1921)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse auto
                                                                                                                                                                                                                                                                                                                                                   Mus
                                                                                                                                                                                                                                                                                                                                                                        AF128117

Mus musculus autoimmune regulator spliced product 1d, complete cds. AF128117

AF128117

AF128117.1 GI:7108535
                                                                                                                                                                                           Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                  Ruan, Q.G., Wang, C.Y., Shi, J.D. and Direct Submission
                                                                                                                                                                                                                                                     regulator gene (Aire)
Unpublished
                                                                                                                                                                                                                                                                                                                                         Mue
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                                                                                                                                                                                                                                                                                                                                         musculus
                                                                                                                                                                                                                                                                                                                                                   musculus (house mouse)
/function="transcription factor"
/note="alternatively spliced pro
/codon_starte1
/product="autoimmune regulator"
                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
                                                                                             map="between D10Mit31 and
                                                                                                           /db_xref="taxon:10090"
/chromosome="10"
                                                                                                                                  strain="B6"
                                                                                                                                                                                ocation/Qualifiers
                                                'gene="Aire"
                                                                       gene="Aire"
                                                                                                                                                                                                                             She, J.X.
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(Aire) mRNA, alternatively
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Best Local Similarity
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71.1%;
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Pred. No. 5e-63;
0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204;
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/db_xref="GI:7108536"

/db_xref="GI:7108536"

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TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTTGAVEGILIQQVFES

GRSKKCIQVGGEFYTPNKFEDDFSGNLKNKARSGSSLKPVVRAKGAGCRDEKVGQQCG

VPPLPSLPSEPQVNQNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSGLWRC

SCCLQGRVQQNLSQPEYSRPPELPAETFILVGLRSASEKTRGPSRELKASSDAAVTTV

NLLAPHPAAPLLESSALCPLLSAGNEGREPGAPSARGSVCGDGTEVLRCAHCAAFHW

RCHFPTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTSGPRPAPGLAKVGDDSASHDP

VLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"

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1049 TCTGGAGATGCTCCTGCTGCCTCCAGGGCAGAGTCCAACAGAACCTGTCCCAGCCTGAGG
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                                                                                                            CTCTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGC
AGTGGGCCATCCAGAGCATGGCCCGTCCGGCGGCCCCCTTCCCCTCCT 1281
                                                                              TTCTACATAGGGACGTGGAGTCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGC
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Ruan,O.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune regulator gene (Aire)
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Archer Road, Gainesville, FL 32610,
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Mus musculus
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Ruan,Q.G., Wang,C.Y., Shi,J.D. and
Direct Submission
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                                    GAGAGGAGGTAAGAGGTCCACCTGGGGAAACCCCTAGCCGGCATGGACACGACTCTTGTCT
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   CAGAGAAAACCAGGGGCCCATCCAGGGAGCTCAAAGCCCAGCTCTGATGCTGCTGTCACAT
                                                                           TGTCCAGGCCCCCGGAGCTACCTGCAGAGACCCCCGATCCTCGTGGGACTGAGGTCAGCTT
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GETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFP
KUDDLNQSRKGRKPLAGPKAAVLPFRPFKFKALLEEPRATPPATLASKSVSSPGSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTPNKFEDPSGNLKNKARSGSSLKPVVRAKGAQVTIPGRDEQKVG
QQCGVPPLLSLDSEDQVNQNEDECAVCHDGGELJCCDGCPRAFHLACLSSPLQEIPSG
QCGVPPLDSLDSEDQVNQNEDBECAVCHDGGELJCCDGCPRAFHLACLSSPLGEIPSG
QCGVPPLDSLDSEDQVNQNEDBECAVCHDGGELJCCDGCPRAFHLACLSSPLGEIPSG
LWRCSCCLQGFVQQNLGQPEVSRPELPAETPILVGLRSASKTTRGPSRELKASSDA
VTYVNLLAPHPAAPLLEPSALCPLLSAGNEGRPGPAPSARCSVCGDGTEVLRCAHCAA
VTYVNLLAPHPAAPLLEPSALCFULSAGNEGRPGPAPGLAKVGDDSA
VTYVNLLAPHPAAPLLEFSALCFULSAGNEGRPGTPGTPGTPGBAVPTSGGRPAPGLAKVGDDSA
VTYVNLLAPHPAAPLLEFSALCFULSAGNEGRPGTPGTPGTPGBAVPTSGGRPAPGLAKVGDDSA
VTYVNLLAPHPAAPLLEFSALCFULSAGNEGRPGTPGTPGTPGTPGTPGTPGTPGTPATGGRPAPGLAKVGDDSA
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/product="autoimmune regulator"
/protein_id="AAP36460.1"
/db_xref="GI-7108532"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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 /rpt_family="Alu" 1251. .1597
                                      447. .616
/note="1/2Aluv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                             /clone_lib="chromosome 21
(Cytometry 7;411-417;1986)
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                           /product="phosphofructokinase"
/note="liver type"
                                                                                                                                                                    /map="21q22.3"
                                                                                                                                                                                         chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                             2586)
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1281 1702

> 1233 1594 1173 1534 1119

1474

1065 1414 1005 1354

PRI

29-APR-1996

Institute,

Euteleostomi;

ORIGIN

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JOURNAL
REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
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AF128121
LOCUS
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KEYWORDS
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Best Local Similarity
Matches 336; Conserv
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Ruan,O.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF128121 1744 bp Mus musculus autoimmune regulator spliced product 2d, complete cds. AF128121
                                                                                                                                                                                                                                                               Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                             2 (bases 1 to 1744)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF128121.1 GI:7108543
                                                                                                                                                                                                                                                                                                                                                        regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus
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2471. .2526
/function="transcription factor"
/note="alternatively spliced pro
/codon_start=1
/product="autoimmune regulator"
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                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /bound_moiety="Sp1"
                                                                                               58. .1524
                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                              'gene="Aire"
                                                                              gene="Aire"
                                                                                                                                                                                       strain="B6"
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100.0%; Pr
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Pred. No. 2.5e-55;
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(Aire) mRNA, alternatively
                                                 product
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                                                                                                                                                                                                                                                                                of Florida, 1600
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JOURNAL REFERENCE AUTHORS TITLE

Unpublished

regulator gene (Aire)

FEATURES

source

/mol_type="mRNA" /strain="B6" organism="Mus musculus" Location/Qualifiers JOURNAL

Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA

о f

Florida,

1600

МS

2 (bases 1 to 1747)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and
Direct Submission

REFERENCE AUTHORS TITLE

Ruan, Q.G., Wang, C.Y., Shi, J.D. and She, J.X. Expression and alternative splicing of the

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (Dases I to 1747)

Mue.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AF128120.1

GI:7108541

Mus musculus

Mus musculus (house mouse)

DEFINITION

AF128120 1747 bp
Mus musculus autoimmune regulator
spliced product 2c, complete cds.
AF128120

mRNA (Aire)

mRNA,

linear ROD 29-F NA, alternatively

29-FEB-2000

Snoo

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RESULT 25
AF128120
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Best Local Similarity
Matches 269; Conserv
                                                                                                      1489 CGCCCGCTGGCCGAGACACCACCCT 1513
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                                                                                                                                                                                              TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
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ilarity 69.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:7108544"
/translation="MAGGDGMLRLIRLHRIEIAVAIDSAFPLLHALADHDVVPEDKF
/ETALKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFP
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TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGGBEYTPNKFEDPSGNLKNKARSGSSLKEVVVRAKQAGBDEQKVGQQCG
VPPLSLPSEPPVNQNEDECAVCHDGGELICOGCPRAFHLACLSPPLGEISGLGKGC
SCCLQGRVQQNLSQPEVSRPPELPAETTGPAESARCSVCGDGTEVLRCAHCAAAFHWR
CHPPTAAARPGTNLRCKSCSADSTFYPGTPGEAVPTSGPRAPGLAKVGDDSASHDPV
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Pred. No. 7.1e-24;
0; Mismatches 104;
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RESULT 26
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                                                                                                                                                SOURCE
                                                                                                                                                                                                      ACCESSION
                                                                         REFERENCE
                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                            DEFINITION
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                                    AUTHORS
TITLE
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Best Local
 JOURNAL
                                                                                                                              ORGANISM
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 1756)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse aut
                                                                                                                                                                                                                     AF128119 1756 bp Mus musculus autoimmune regulator spliced product 2b, complete cds.
regulator gene (Aire) Unpublished
                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                    AF128119.1 GI:7108539
                                                                                                                                                                                                      spliced product
AF128119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCCGCTGGCCGAGACACCACCCT
                                                                                                                                                                                                                                                                                                                                                                                          CGTCCGGCGGCCCCCTTCCCTCCT 1281
                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCCTTCTGAGCGAGCACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCC 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCAA-----GGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAG
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GETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYMLERYSRLHSILDGFP
KDVDLNQSKKGRKPLAGPKAAVLPFRFPTKRKALEEPRATPPATLASKSYSSPGSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVFGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTPNKFEDPSGNLKNKARSGSSLKPVVRAKGAQGRDEQKVGQQCG
VPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCFRAFHLACLSPPLQEIFSGLWR
CSCCLQGRVQQNLSQPEVSRPPELPAETPFPAFSARCSCCDGTEVLRCAHCAAAFHW
RCHFPTAAARFGTNLRCKSCSADSTFPTFGTFGBAVFTSGFRPAFGLAKVGDDSASHDP
VLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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/function="transcription fact
/note="alternatively spliced
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/product="autoimmune regulator"
/protein_id="AAP36465.1"
/db_xref="GI:7108542"
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Pred. No. 7.1
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(Aire) mRNA, alternatively
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RESULT 27 AF128118 LOCUS

DEFINITION

AP128118 1759 bp
Mus musculus autoimmune regulator
spliced product 2a, complete cds.
AF128118

mRNA (Aire)

mRNA, alternatively linear

ROD 29-FEB-2000

ACCESSION

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REFERENCE
AUTHORS
TITLE
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Ruan,Q.G., Wang,C.Y., Shi,J.D. and i
Direct Submission
Submitted (12-FEB-1999) Pathology, 1
Archer Road, Gainesville, FL 32610,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCC
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/product="autoimmune regulator"
/product="alf36464.1"
/protein_id="AAF36464.1"
/db_xref="Gl:7108540"
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/bTTRLKEKEGCPQAFHALLSWILTRDSGAILDFWRILFKDYNLERYSRLHSILDGEF
KDVDLNQSRKGRKPLAGPKAAVLPFRPTKRKALEERPAFPLAGKSVSSPGSHK
TKPPKKEDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTPNKFEDPSGNLKNKASGSSLKEVVRAAGAQVTIGRDEQKVG
QQCVPPLFSLDSEQVQNLSQPEVSRPPELPAEIFGFPGAPHLACLSPFLQEIFKQ
QQCVPPLPSLDSEQVQNLSQPEVSRPPELPAEIFGFPGBAVFLACLSPFLQEIFG
QQCVPPLPSLDSEQSTNLRCKSCSADSTFTFGTFGBAVFTSGDRFAFHLACLSFDLGAAA
LFHWRCHFFTAAARFGTNLRCKSCSADSTFTFGTFGBAVFTSGFRPAFGLAKVGDDSAS
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58. .1536
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/note="alternatively spl;
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/mol_type="mRNA"
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Submitted (12-FEB-1999) Pathology, University of Florida, 1600
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Ruan, O.G., Wang, C.Y., Shi, J.D. and She, J.X.
Expression and alternative splicing of the mouse autoimmune
regulator gene (Aire)
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Ruan, Q.G., Wang, C.Y., Shi, J.D.
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Mammalia; Eutheria; Rodentia;
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                                                                                        TCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCC
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TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
                                                                                                                                                                                     GCCAAGGTAGGGGACGACTCTGCTAGTCACGACCCTGTTCTACATAGGGACGACCTGGAG
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/product="autoimmune regulator"
/product="autoimmune regulator"
/protein_id="AAF15463.1"
/db_xref="GI:7108538"
/db_xref="GI:7108538"
/td_xref="GI:7108538"
/td_xref="G
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/function="transcription factor"
/note="alternatively spliced pro
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/mol_type="mRNA"
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Pred. No. 7.1e-24;
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Mus musculus autoimmune regulator
spliced product 3c, complete cds.
AF128124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulator gene (Aire)
Unpublished
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                                                                                                                                   CCAGGTTAACCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGGAGGTGAGCTCAT
                                                                                                                                                                      TTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCAT 571
                                                                                                                                                                                                                                              TGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTGCATGGGCGTCTC 511
GATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCA 691
                                                                                    CTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCTCTCCCCTCCGCTCCGGGA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCCGCTGGCCGAGACACCACCCT 1528
                                                            CTGTTGTGACGGCTGTCCCCGGGCCTTCCACCTGGCCTGTCCCCCACCTCTGCAGGA
                                                                                                                                                                                                             cerceececccccrccrccrcir 1281
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                             /product="autoimmune regulator"
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/db_xref="GI:7108550"
/tanslation="MAGDCWLRRILIRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
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/translation="MAGDCWLRRILIRDSGAILDFWRILFKDYNLERYSRLHSILDGFP
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GRSKKCIQVGGEFYTBWKFEDPSGNLKNKARAGGSSLKPVVRAKGAQGRDEQKVGQQCES
GRSKKCIQVGGEFYTBWKFEDPSGNLKNKARAGGSSLKPVVRAKGAQGRDEQKVGQQCE
VPPLFSLPSEQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSGLWR
CSCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQILLCRLDSHARHTGRSCTHLWAP
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58. .1275
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/mol_type="mRNA"
/strain="B6"
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Pred. No. 7.8e-21;
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                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 213; Conserv
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  930
                                512 TIGCCIGIGCCAGAAGAATGAGGACGAGIGIGCCGIGIGIGIGGGACGGGGGAGCICAI 571
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Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF128122 1637 bp
Mus musculus autoimmune regulator
spliced product 3a, complete cds.
AF128122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-FEB-1999) Pathology, University of Florida, 1600 Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCCCAGCCTGAGGTGTCCAGGCCCCCGGAGCTACCTGCAGAGACCCCGGACCAATCTCC 1157
CCAGGTTAACCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGGAGGTGAGCTCAT
                                                                                                                TGGGAAGGAGGTGCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTGCATGGGCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 1637)
un,Q.G., Wang,C.Y., Shi,J.D. and
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       754
                                                                                                                                                                                                                                                                                                        QETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFPKDVDLNQSRKGRKPLAGPKAAVLPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVPESGRSKKCIQVGGFYTPNKFEDPSGNLKNKARSGSSLKPVVRAKGAQVTIPGRDEQKVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Aire"
58. .1287
                                                                                                                                                                                                                                                     LWAPSSTWACQGRGRLC"
                                                                                                                                                                                                                                                                      QQCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQILLCRLDSHARHTGRSCTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    map="between D10Mit31 and D10Mit10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:10090"
chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                         translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain="B6"
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                                                                                                                                                                       10.3%;
                                                                                                                                                     0;
                                                                                                                                                     Score 159; DB 10;
Pred. No. 7.8e-21;
0; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
(Aire)
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                                                                                                                                                                                         Length 1637;
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                                                                                                                                                     Gaps
                                                                          929
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526 AGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCT

Matches 179;

Conservative

0,

Mismatches

50;

Indels

0;

Gaps

0;

Query Match Best Local Similarity

9.6%;

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AUTHORS
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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AF128125
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                                                            ORIGIN
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AF128125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-FEB-1999) Pathology, University of Florida, 1600 SW
Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruan, Q.G., Wang, C.Y., Shi, J.D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, 1 (bases 1 to 1622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCCCCAGTGGCCTCTGGAGATGCTCCTGCTGCCTCCAGGGCAGAGTCCAACAGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACACTCCAGGAGGTGCA 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTTGTGACGGCTGTCCCCGGGCCTTCCACCTGGCCTGTCCCCCACCTCTGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Road, Gainesville, FL
Location/Qualifiers
                                                                                                                 /translation="maggdgmlrrllrhrteiavaidsafpllhaladhdvvpedkf

@stlrlkækegcpoafhallswilterdsgaildfwriifkoxileerysrhesildgfp

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vpplpslpslpsepqvnonedecavchdogeliccdgcprafhlaclspploeipsgrurc
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                                                                                                 SCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQILLCRLDSHARHTGRSCTHLWAPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="B6"
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                                                                                                                                                                                                                                                                                                                'note="alternatively spliced product
                                                                                                                                                                                                                                                                                                                                                                                           'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                map="between"
                                                                                                                                                                                                                                                                                                                                      function="transcription factor"
                                                                                                                                                                                                                                                                                                                                                         'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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Score 149; DB 10;
Pred. No. 6.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                      D10Mit31 and D10Mit10"
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                    Length 1622;
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                                                                         Query Match
Best Local S
Matches 179
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TITLE
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Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spliced product 3b, complete cds. AF128123
AF128123.1 GI:7108547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archer Road, Gainesville, FL
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-FEB-1999) Pathology, University of Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1634)
Ruan, Q.G., Wang, C.Y., Shi, J.D. and
Direct Submission
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Mus musculus autoimmune regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulator gene (Aire)
Unpublished
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                                                                                        Similarity
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               AGAACGAGGATGAGTGTGCCGTGTGCCACGACGGAGGTGAGCTCATCTGTTGTGACGGCT
                                           AGAATGAGGACGAGTGTGCCGTGTGTCGGGACGCGGGGAGCTCATCTGCTGTGACGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (house mouse)
                                                                          Conservative
                                                                                                                                                                           /translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
GETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFP
KDVDLNQSRKGRKPLAGPKAAVLPFRPTKRKALEEPRATPATLASKSVSSPGSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTPNKFEDPSGNLKNKARSGSSLKPVVRAKGAQVTIPGRDEQKVG
QQCGVPPLPSLPSEPQVNQNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSG
QQCGVPPLPSLPSEPQVNQNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSG
                                                                                                                                                                                                                                                                                                                                                                            /gene="Aire"
58. .1284
                                                                                                                                                  LWRCSCCLQGRVQQNLSQPEVSRPPBLPAETPDQSPLQILLCRLDSHARHTGRSCTHL
WAPSSTWACQGRGRLC"
                                                                                                                                                                                                                                                                 /codon_start=1
/product="autoimmune regulator"
/protein_id="AAF36468.1"
/db_xref="GI:7108548"
                                                                                                                                                                                                                                                                                                                            /function="transcription factor"
/note="alternatively spliced pro
                                                                                                                                                                                                                                                                                                                                                                                                                     map="between D10Mit31 and D10Mit10"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/chromosome="10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                             'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _type="mRNA"
                                                                                     9.6%;
78.2%;
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                                                                       Score 149; DB 10;
Pred. No. 6.9e-19;
0; Mismatches 50;
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(Aire)
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                                          REFERENCE
AUTHORS
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Query Match
Best Local Similarity
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AX344994
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                            Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with Patent: WO 0200928-A 66 03-JAN-2002;
                                                                                                                       synthetic construct synthetic construct
                                                                                                                                                                                             Sequence 66 from Patent AX344995
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              Epigenomics AG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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location/Qualifiers
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Pred. No. 4.7e-13;
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SOURCE
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Best Local Similarity
Matches 139; Conserv
             Query Match
Best Local Similarity
Matches 119; Conserv
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BV089377

BV089377.1 GI:37666856
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Usuka,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A.,
McPherson,J.D., Foernzler,D. and Peltz,G.
Mus musculus SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BV089377 581 bp DNA linear STS 15-OCT-200 RPAMMSEQ0001273 Roche Palo Alto Mus musculus STS genomic, sequence
                                                                                                                                                                                                                                                                            Primer A: No primer submitted.
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Jonathan Usuka
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
                                                                                                                                                                                                                                                                                                             Email: Jonathan.Usuka@roche.com
                                                                                                                                                                                                                                                                                                                                        3431 Hillview Ave, Mailstop S3-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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             Conservative
                                                                                                                                                                                                                                                                                                                                                        Palo Alto
Palo Alto
                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
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/mb_xref="taxon:10090"
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/clone_lib="Roche Palo Alto"
/clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15 different strains-of mice (as of October 1, 2003). Those strains include AJJ, A/HeJ, -129/5v, AXR/J, B10.D2-H2/oSnJ, BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J, MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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             ;
             Score 96.6; DB 11
Pred. No. 1.3e-08;
0; Mismatches 19
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Pred. No. 8e-10;
0; Mismatches
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Sciurognathi; Muridae;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; I (Dases 1 to 1835)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y Detter,J.C. and She,J.X.
Chromosomal localization and complete genomic sequence murine autoimmune regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-NOV-1998) Department of Pathology, Laboratory Medicine, University of Florida, 1600 Room D6-15, Gainesville, FL 32610, USA Location/Qualifiers
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.Q.,
Detter,J.C. and She,J.X.
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AJ007715.1 GI:3550507
Alre gene; autoimmune regulator.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAGCTCATCTGTTGTGACGGCTGTCCCCGGGCCTTCCACCTGGCTTGCCTGTCCCCAC 10469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 18616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(1347. .2537,5851. .6020,6085. .6232,6233, .6296,7758. .7893,10146. .10356,10359. .10551, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .10541, .105
/rpt family="SINE/B4"

join(2970. .3416,3417. .3591,3592. .3820,3821. .3976,

3977. .4357,4358. .4432,4433. .4879,4880. .4993,4994. .6413,

3977. .4357,4358. .6750,6751. .6831,6832. .8505,8506. .8621,

6414. .6562,6563. .6750,6751. .6831,6832. .8505,8506. .8621,

8622. .9709,9710. .9809,9810. .10660,10661. .10837,

10838. .11786,11787. .11908,11909. .12004,12005. .12113,
                                                                                                                                                                                                                                                                          comp.
                                                                                                                                                                                                                                                                                                                                                          complement (2281. .2291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Aire"
complement(1347. .1546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="129sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%;
85.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                          family="DNA/MER1_type"
lement(1912. .2128)
                                                                                                                                                                                       family="SINE/Alu"
Tement (2425. .2537)
                                                                                                                                                                                                                                                                          family="SINE/B4"
lement(2292. .2424)
                                                                                                                                                                                                                                                                                                                                                                                         family="SINE/B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 96.6; DB 10;
Pred. No. 7.4e-09;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD 11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scott, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
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                                  intron
                                                                                                                                                                                                                                                                          repeat_unit
                                                                                                                                                                                                                                                                                                                                                          repeat_unit
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                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
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                                                                                                                                                                                                                                                                            /rpt_family="SINE/B2"
complement(6085. .6232)
                                                                                                                                                                                                                                                                                                                                                             complement (5851. .6020)
                                                                                                                                                                                         complement (6233. .6296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4433. .4879
/gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3015. .3416
/gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <2970. .3104
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                                                                                                                                                                                                                                                                                                                                /gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                               1994. .6413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number=5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1358. .4432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9592. .3820
gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16835. .16985)
                                                         number=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417. .3591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6166. .16246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number=2
                                                                                                                                                                                                                            family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4357
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TKPPKKPGGHLSGGHLFGNGIOTMAASVORAVTVASGDVGTRGAVEGILJOQVFES
GRSKKCIQVGGEFYIPNKFEDDPSGNLKNKARSGSSLKPVPRAKGAQVTIPGRDBQKVG
QCGVPPLPSLPSEDPSGNLKNKARSGSSLKPVPRAKGAQVTIPGRDBQKVG
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QCGVPPLPSLPSEDPSGNLKNKARSGSSLKPVPRAKGAQVTIPGRDBQKVG
QCGVPPLPSLPSEDPSGNLKNKARSGSSLKPVPRAKGAQVTIPGRDBQKVG
QCGVPPLPSLPSEDPSGNLKNKARSGSSLKPVPRAKGAQVTIPGRDBQKVG
QCGVPPLPSLPSEDPAFPLASTPPILVGLKASASSUK AAPHWRCHFPTAAARPCTNLECKSCSADSTPTCTGGLAVETSGRPAPGLAKVGDDS
ASHDPVLHRDDLESLLNEHSPDGILQMAIQSMSRPLAETPPPSS"
AAPHWRCHFPTAAARPCTNLRCKSCSADSTPTCTFGEAVPTSGRPAPGLAKVGDDS
ASHDPVLHRDDLESLLNEHSPDGILQMAIQSMSRPLAETPPPSS"
//www.barrel"
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exon

intron

Length 18616; Indels

1.

Gaps

8602 621 8542 561 ۳.

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/number=6
6751. .6831
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/rpt_family="SINE/Alu"
9710. .9809
                                                                                                                                                          complement (12262.
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/rpt_family="SINE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="SINE/B2"
complement(10359...10551)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6832. .8505
/gene="Aire"
                                        complement (12432. .12626)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (11453. .11562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (10146. .10356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8622. .9709
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                                                                         gene="Aire"
                                                                                        /rpt_family="LTR/MaLR"
complement(12415. .12431)
                                                                                                                                             complement (12277. .12408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Aire"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9810. .10660
/gene="Aire"
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7027
                                                                                                                            gene="Aire"
                                                                                                                                                                                                                  number=12
                                                                                                                                                                                                                                                                                      |2005. .12113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1060. .11182
gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number=10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10838. .11786
gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number=9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="Aire"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number=7
                                                                                                                                                                                                                                   gene="Aire"
                                                                                                                                                                                                                                                                    number=12
                                                                                                                                                                                                                                                                                                                       number=11
                                                                                                                                                                                                                                                                                                                                                                                             gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0661. .10837
                                                                                                                                                                                                                                                     2114. .14604
                                                                                                                                                                                                                                                                                                                                           gene="Aire"
                                                                                                                                                                                                                                                                                                                                                          1909. .12004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number=10
                                                                                                                                                                                                                                                                                                                                                                            number=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="SINE/B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _family="SINE/B4"
_ .7160
                                                          family="SINE/B2"
                                                                                                                                                             family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                family="LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="SINE/B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="SINE/B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7159
                                                                                                                                                                                                .12378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
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SOURCE
ORGANISM
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Submitted (22-UIN-1998) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers
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46872 bp DNA linear ROD 05-AUG-19: Mus musculus cosmid MPMGc121L12287 containing the syntenic region of the human AIRE gene, complete sequence.
                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 46872)
Blechschmidt, K., Huong-My, C., Nordsiek, G., Drescher, B., Rosenthal, A. and Yaspo, M.-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Blechschmidt, K., Schweiger, M., Wertz, K., Poulson, R., Christensen, H.M., Rosenthal, A., Lehrach, H. and Yaspo, M.L. The mouse Aire gene: comparative genomic sequencing, gene organization, and expression genome Res. 9 (2), 158-166 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An autoimmune disease, APECED, caused by mutations in a novel gene featuring two PHD-type zinc-finger domains. The Finnish-German APECED Consortium. Autoimmune Polyendocrinopathy-Candidiasis-Ectodermal Dystrophy Nat. Genet. 17 (4), 399-403 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46872)
Aalronen,J., Bjoersee,P., Perheentupa,J., Horelli-Kuitunen,N., Palotie,A., Peltonen,L., Lee,Y.S., Francis,F., Hennig,S., Thiel,C., Lehrach,H. and Yaspo,M.-L.
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99148139
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/note="GRAIL, gcore = 99.000%, comment = excellent"
/evidence=not_experimental
complement(156..316)
                                                     /note="GenScan, score = 14.95%,
172 bp frame: 2 phase: 1"
/evidence=not experimental
complement(156. .327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (12627. .12769)
                                                                                                                         complement (156. .327)
                                                                                                                                                        /db xref="taxon:10090"
/note="Cosmid MPMGc121L12287 originating from cosmid
library number 121 (RZPD-berlin). Cloning vector Lawrist
                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129/Ola"
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85.6%;
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Pred. No. 7.4e-09;
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וספב	<pre>/evidence=not_experimental 32433410 /note="homology = 59.50%, score = 26, counts = 28" /evidence=not experimental</pre>	/evidence=not_experimental complement(3128 . 3163) /note="MZEF, score = 75.9%"	/evidence=noc_experimental complement(3128. 3173) /note="GRAIL, score = 94.000%, comment = excellent"	/note="GenScan, score = 3.08%, comment = Internal_exon 46 bp frame: 2 phase: 1"	410	complement(23552441) /note="GRAIL, score = 88.000%, comment = excellent" /evidence=not experimental complement(29523023)	hase: 0"	<pre>/note="GRAIL, score = 64.000%, comment = good" /evidence=not experimental complement(23552441) /note="GenScan, score = 5.24%, comment = Internal exon 87</pre>	imental 318)	00%, comment = ex	/note="MZEF, score = 79.6%" /evidence=not experimental complement/9079 2123	by frame: 0 phase: 0" /evidence=not_experimental	t family="AluJ/FLAM" plement(20792318)	/evidence.not experimental complement(18051885)	/ryt_family="Alusp" 1595. 1669 /rote="MZEF acore = 01 3%"	/evidence=not_experimental complement(15721634) /evidence=not_experimental	/ evidence=not experimental complement(11291208) /note="MZEF, score = 57%"	/evidence=not experimental complement(1129. 1208) /note="GenScan, score = 3.57%, comment = Internal_exon 80 hn frame: 0 phase. 2"		/evidence=not experimental complement(9351047) /note="MZEF, score = 96.5%"	×	/note="Xpound exon prediction, score = 93% (0%)"
	exon	repeat_region	repeat_region	repeat_region	repeat_region	exon	exon	٠	exon	exon		exon	gene	misc_feature	repeat_region	exon	exon	repeat_region	repeat_region	misc_feature	exon	
990)" Perimental	erimental C"	0 > >	/evidence=not_experimental /rpt_family="fgNa-Cys-TGC" complement(12664 12819)	/rpt family="MITID" (complement(1253912600)	/evidence=experimental complement(1224112306) /evidence=not experimental	/evidence-experimental 1146511578 /gene="Mouse homologue of the human APECED gene (AIRE; ACC. No. 227990)" /number=5	1094311017 /gene="Mouse homologue of the human APECED gene (AIRE; Acc. No. 297990)" /number=4	2 7 7 .=		/GYLUCIUS TO APECED JOING (AIRE; 1000210176 / Jene-"Mouse homologue of the human APECED gene (AIRE; Acc. No. Z97990)"	/geide="mouse nomologue of the numan AFECED gene (AIKE; Acc. No. 297990)" /number=1 /oriderocomocifacts1	or the numan AFECED gene	imental	/:bccamily="Artus9" 9395. 9666 /note="CpG_island score = 0.74, GC = 63.20%, CpGs = 25;		77947905	<pre>/ ipc _tamily="Aluoo" complement(77337878) /note="GRAIL, score = 57.000%, comment = good shadow" /evidence=not experimental</pre>		/note	/ HOLE - SMALL, SCORE - 30.000%, Comment - 9000 /evidence=not_experimental 4343. 4367 /standard name="gan"	ental	/note="GenScan, score = 1.75%, comment = Initial_exon 129

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AC015891
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Lifect Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome AL Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 158049)

Birren, B., Nubbaum, C., Lander, B., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cock, A., Cook, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Hortcon, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jindblad-Toh, K., Liu, G., MacLean, C., Madchand, P., Major, J., Mathews, C., McCarthy, M., Medrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Severy, P., Smith, C., Spencer, B., Schupback, R., Stenaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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1 (bases 1 to 158049)
Birren, B., Nusbaum, C. and Lander, E.
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HTG; HTGS_PHASE1; HTGS_FU
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85.6%; Pred. No. 6.4e-09;
ative 0; Mismatches 19
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                                                                                                                                                                                          RESULT 39
                                                                                      ACCESSION
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                                                                                                                                                   POCUS
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                                                                                                                                                                                                                                                                                                                                          152916
AC138672

Mus musculus chromosome 10 clon
SEQUENCE, 13 unordered pieces.
AC138672
AC138672.3 GI:29150492
HTG; PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)

Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                   562
                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 TGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGTCCGGGACGGCG
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Submitted (20-NOV-2002) Whitehead Institute/MIT Center for Genome Submitted (20-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 20, 2002 this sequence version replaced gi:25046447.
All repeats were identified using RepeatMasker:
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                        GTGAGCTCATCTGTTGTGACGGCTGTCCCCCGGCCTTCCACCTGGCTTGCCTGTCCCCAC
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Center clone name: 522_L_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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5: gap of 100 bp
3: contig of 16858 bp in length
7: gap of 100 bp
7: gap of 100 bp in length
7: gap of 100 bp
5: contig of 28878 bp in length
5: gap of 100 bp
5: contig of 28878 bp in length
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2: contig of 36517 bp in length
2: gap of 100 bp
9: contig of 14207 bp in length.
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, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Dases 1 to 19001s)

Research, 320 Charles Street, Cambridge, MA 02141, USA (Charles, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boyuslawkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., O'Neil, D., O'Neil, D., Schupsack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Stubs, M., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2003 this sequence version replaced gi:28394987. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Birren, B., Nusbaum, C.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Birren, B., Nusbaum, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemierry: Dye-cerminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 186501 bases at least Q30 Consensus quality: 18797 bases at least Q30 Consensus quality; 188318 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 411 J
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                                                                                                                                            /note="assembly_fragment"
167205. .190019
                                        clone_end:T7
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                note="assembly_fragment/
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167104: contig of 26336 bp
167204: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11865:
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contig of 1594 bp in length
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of 3644
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of 2227 bp in length
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AC108592/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Allen,C., Allen,H., Alsbrooke,S., Amin,A., Anguiano,D.,
Allen,C., Allen,H., Alsbrooke,S., Amin,A., Anguiano,D.,
Anyalebechi, W., Aoyagi,A., Ayoegi,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Byth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,Z.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eave,K.,
Eggan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,B., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Hernandez,R., Hines,S., Hladnn,S.L., Hodgson,A., Hernandez,J.,
Hernandez,R., Hines,S., Hluyk,S., Hame,J., Idlebird,D., Jackson,L., Jaccb,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Maheshwari,M., Mahretin,K., Martin,R., Martinez,B.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,B.,
Mangum,B., Mapua,P., Martin,R., Martin,R., Martinez,B.,
Nankervis,C., Nall,P., McNeill,T.Z., Meenen,E.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pul,L-L.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pul,L-L.,
Plazo,M., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 TGGGCGTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCG
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC108592
AC108592.5 GI:25006698
HTG; HTGS_PHASE1; HTGS_DRAFT; I
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus clone CH230-144C19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGTCCCTCTTGCCTG-GTCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCCTGTCCCCTC 621
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Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejog, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Willson, R., Weins, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Yon Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission Direct Submission Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (1998) (USA) (
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Contac

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RESULT 41
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Best Local
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                                                                                                                                                                                                                                   AUTHORS
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooka, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
                                                                                                                                                                                                                                                                                                                                 AC109383
AC109383.5 GI:25006726
HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC109383 283951 bp DI Rattus norvegicus clone CH230-48B22,
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                            Rattue
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                                                                                                                                                                                                                                                       (bases 1 to 283951)
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212890
214331
214431
215740
215840
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214330: contig of 1441 bp in length
214330: gap of unknown length
21439: gap of unknown length
215739: contig of 1309 bp in length
215839: gap of unknown length
217688: contig of 1849 bp in length
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="wgs_contig"
87246. .89004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="wgs_contig"
71480. .74410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_contig"
189782. .190939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_cor
10093. .11330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="wgs_contig"
177890. .179119
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175878. .177789
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154433. .155684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_contig"
|70990. .172417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .60679.
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84.9%;
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.161680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear HTG 15-NOV-2002
SEQUENCING IN PROGRESS
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COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Project Information

Center code: BCM

Center: Baylor College of Medicine

Center project name: GPWN Center clone name: CH230-4

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Pernandez, S., Finley, M., Plagg, N., Forbes, L., Foster, M., Gabisl, A., Ganta, R., Garcia, A., Garrer, M., Gebregeorgis, E., Gebre, K., Gill, R., Grady, M., Guerra, W., Gebregeorgis, E., Gebre, K., Gill, R., Grady, M., Guerra, W., Gebregeorgis, E., Gebre, K., Gill, R., Grady, M., Guerra, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerara, W., Harnandez, J., Hines, S., Hladun, S.L., Hodgeon, A., Hogues, M., Hernandez, J., Hines, S., Hladun, S.L., Hodgeon, A., Hogues, M., Hernandez, J., Jackson, A., Jackson, A., Jackson, A., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kally, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., London, P., Lozado, R. J., Lu, X., Ma, J., Liu, J., Liu, Y., London, P., Lozado, R. J., Lu, X., Ma, J., Liu, J., Liu, Y., London, P., Lozado, R. J., Lu, X., Ma, J., Liu, J., Lorenshewa, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, J., Liu, J., Lorenshewa, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, J., Liu, Y., Lorenshewa, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, J., Liu, Y., Lorenshewa, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, J., Liu, Y., Lorenshewa, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, J., Liu, Y., Lorenshewa, L., London, P., Mahmoud, M., Mathmoud, M., Mahmoud, M., Martin, R., Martin
                         Direct Submission

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23677016.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 283951)
shotgun sequence only table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished 2 (bases 1
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RESULT 42
BV163805
                    KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                               22989 CAGAAGAACGAGGATGAATGCGCTGTGTGCCATGACGGAGGCGAGCTCATCTGCTGTGAC
                                                                                                                                                                                                                                                                                                                                                     522 CAGAAGAATGAGGACGAGTGTGCCGTGTGTCCGGGACGGGGGGAGCTCATCTGCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                           101;
                    STS
                                                                          tagged site.
BV163805
                                                                                                                   BV163805 558
RPAMMSEQ0036732 Roche Palo Al
Mus musculus
                                                            BV163805.1 GI:47270013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length

(see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 5 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
                                                                                                                                                                                                                                      GGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGGAGATCCCCAG 640
                    musculus
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17198
93016
93116
162411
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281692
281792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wgs_end_extension
clone_end:Sp6"
91231. .93015
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/note="clone_boundary
clone_end:Sp6
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803. .35510
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clone_end:Sp6"
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/mol_type="genomic DNA"
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17197: gap of unknown length
93015: contig of 75818 bp in length
93115: gap of unknown length
162410: contig of 69295 bp in length
162510: gap of unknown length
281681: contig of 119181 bp in length
281791: gap of unknown length
283951: contig of 2160 bp in length.
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84.9%;
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40. .90031
                    (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 90.2; DB 2;
Pred. No. 8.4e-08;
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                                                                                                                   Mus musculus
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BV089350
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Best Local Similarity
                                                                                                                                                                                                        AUTHORS
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1 (bases 1 to 574)
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                                                                                                                                                                                                                                                                                                                                                       tagged site.
BV089350
                                                                                                                                                                                                                                                                                                                                                                                          BV089350 574 bp
RPAMMSEQ0001246 Roche Palo Alto
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Roche Palo Alto
3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA:
Tel: 6508555807
                                                                         Contact: Jonathan Usuka
Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
                                                                                                                                                                  Usuka,J., Liao,G., Cheng,J.,
McPherson,J.D., Foernzler,D.
Mus musculus SNPs
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 558)
                                    3431 Hillview Ave, Mailstop S3-1, Tel: 6508555807
                                                                                                                                                Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                     BV089350.1
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Primer A: No primer submitted
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                   Jonathan. Usuka@roche.com
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/clone lib="Roche Palo Alto"
/rothe="Roche Palo Alto"
/note="Sups developed from assay sequences derived from 15
different strains of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ, 129/Sv, AKR/J, B10.D2-H2/OSnJ,
BALB/CB/J, BALB/CJ, C3H/HeJ, CSTPL/GJ, CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei."
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Pred. No. 7e-06;
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and Peltz, G.
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us STS (
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BV088992
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Matches 100;
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Usuka,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A., McPherson,J.D., Foernzler,D. and Peltz,G.
Mus musculus SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S93 bp
RPAMMSEQ0000888 Roche Palo Alto
                                                                                                                                                                                                                                   Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BV088992.1 GI:37666471
STS.
                                                                                                                                                                                                                                                                                     3431 Hillview Ave, Mailstop S3-1,
Tel: 6508555807
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Roche Palo Alto
                                                                                                                                                                                                                                                                                                                                                      Contact: Jonathan Usuka
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
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Location/Qualifiers
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                               /clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15
/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ,-129/Sv, AKR/J, B10.D2-H2/OSnJ,
BALB/CByJ, BALB/CJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.-"
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/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ,-129/Sv, AKR/J, B10.D2-H2/OSnJ,
BALB/CByJ, BALB/CJ, C3H/HeJ, C57BL/6J,-CAST/Bi, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Bi.-"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/map="10.7948-7452-CAAA01111727.1.1.11206"
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/db_xref="taxon:10090"
/map="10-7927-7476-CAAA01111727.1.1.11206"
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77.5%;
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Pred. No. 7e-06;
0; Mismatches 29;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 155020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens junctophilin 3 (JPH3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-OCT-2001) Psychiatry, Institutions, 600 N. Wolfe St., Bal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \label{eq:holmes} \begin{tabular}{ll} Holmes, S.B., & Ingersoll-Ashworth, R.G., & Ross, C.A. & and & Margolis, R.L. \\ Direct & Submission \\ \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                               /gene="JPH3"
/product="junctophilin 3"
complement(<36507. .36887)
/gene="JPH3"
                 /codon_start=1
/product="junctophilin 3"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/db_xref="d1:17646245"
/translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
/translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
HGFEYLGVYTWPSGNTYQGTWAQGKAHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
                                                                                                                                                                    membrane and endoplasmic
                                                                                                                                                                                                                                                                                                                  /note="synonym: JP3"
complement(<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                                                                    /rpt_unit="ctg"
complement(<36507. .>36887)
NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                                       /note="component of the junctional complex between plasma
nembrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                  /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       _type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type="genomic DNA"
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77.5%;
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Pred. No. 6.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 18-JAN-2002
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Euteleostomi;

Hwang, H.S.,

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RESULT 46
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     POCUS
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Best Local Similarity
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AF429315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSCYKSYYMMARSKRMKGMKWGRCWGSMWGSASRSSCYKCYKSMRCSMMSSKCYRCAGCM 17418
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                                                                                                                                     SSMSCTSMYRCCWGGMKSYSTCGTTCKKCTGYKKSRTWYWWMYSWTSKWYMWR 1783
                                                                                                                                                                                                                                                                                                  TTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAACCCTGCCCCACTTCTCTACTC
                                                                                                                                                                                                                                                                                                                                                        KSASRSSWCSRRMKGMRGSCWSSKMWGGSRSRSASSKCKGSRGMRRRSKRSSKYRKRGRG
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                                                                                                                                                                                                                                               KKRSMTKSKGSKGKSKCWKRSGSMTSSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACCY
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 4.8%; Score 73.6; DB 9; Local Similarity 11.3%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                           17859 KGWCMYTGKSKKGKKYYASKRGRKKGTTYWKRKMSAWSRKWWRWAYSMMRCAGWMGAACG
                                                                                                                                                                                                                                                                                                                                                                                                            209 GGCCCCACTGCCCTGTGAGGAAGGGTTCATGTGGTTGGTGTACAGTTCCGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A Potter, N.T., Ross, C.A. and Margolis, R.L. A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 125020)
Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF429315.1
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                      WGSCYKCMKYYSGWSSYSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRKRSYYYWGGG
                                                                               GCATGGGAGCAGGGCAGAGACTGGGGAGTTCAGGTACCCAGAGATGCTGCTGGGGGAGCT 447
                                                                                                                                     SYMWGMSMCMSCMSMAKSYMMCYCYMYRMSSYMSYYYKCYSCMGMSSTSYSYSCCWKMSS
                                                                                                                                                                                      CTGTTCGAGACÇAG-ATGGATGGGGAACAGGTGGTCAGGGCAGAATTTCAGGCCCTGGCA 387
                                                                                                                                                                                                                                               ASRSMKCCWGGYRKSAGSKSSRGGTGYYMKKKGGGKGSMSSKKWKGSSTSRRRGSSAKSC 17740
                                                                                                                                                                                                                                                                                                  AACGCAGCAGCCTGCAAGAAACCGGGTTTTCTTCCCAATAGGGATGGCCCCGGGGGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 452; Mismatches 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
/translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGFKGQGEYTGSWS
HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: JP3"
complement(<36507. .>36887)
/gene="JPH3"
/product="junctophilin 3"
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/gene="JPH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="16"
/map="1624.3; between D16S520 and WI-12410"
/mate="160lated from a patient with Huntington's Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type=tandem
/rpt_unit="ctg"
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|mol_type="genomic DNA"
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Submitted (11-FEB-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 11, 2004 this sequence version replaced gi:42517008.
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprindormes; Cyprindae; Danio.
                                                                                                                                                                                                                                                Danio rerio (zebrafish)
Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                         complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Zebrafish DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                         BX649390
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                                                                                                                          Johnson, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMCWWYYMKSWGYKRYKRCCMKKKGCTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWG 17382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMBSRSBSKVKSKWSMSRRGKYYYCTDSMKKMYYTGC 16871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCTTC 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCCCCAGCCCGCCCGCCTGGCCCTGGCCAAGGATGACACTGCCAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGTGGRYKGGGRSYGKGGGSYKGGGSWGGKGGKSTRGSSAGKKS----SYKKMSCCARYK 16968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGGGCCTGCGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRSMCCMCMCKSCCGCYSMGMSSYSYSGKYSWGMKSYMWRSYYSKRS---TSKAWRSSKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKTSYSAKGSGRGCYYCWGWGRKGRKCMSSRKMKMYKSYYRRKRWMTCMKMCYSMYMAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGCTCCTGGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - TGGACACGACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAGCCCGGGCAGAGGAGCCCCGGGAGCCACCCGTGGAGACCCCGCTCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMSYSKCYSRWMWCMSYYYCWGGKCWSSCWWSSMRKKSKGGSWAKGMVWDKGSVSTDKSD 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGG
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DKEY-261L2 in l:
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one-plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession mumbers given in the feature table with their source databases:

Em: RMBL; Sw:, SwiSSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where either ited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                4966 bp mRNA linear i
Homo sapiens cDNA FLJ45103 fis, clone BRAWH3032571, n
similar to Chromodomain helicase-DNA-binding protein
AK127046
         Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H. Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A.,
                                                                                                                                                                                        AK127046.1 GI:34533779 oligo capping; fis (full insert Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-261L2
is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: zfish-help@sanger.ac.
                                                                                                    Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="DKK1-2014"
/clone_lib="DanioKey"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-261L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .. .184594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5%;
74.6%;
                                                                                                    Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70; DB 5;
Pred. No. 0.00077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                        sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184594;
                                                                                                    Hominidae;
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Inagaki,H.,
                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                               moderately
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                                                                                                          Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                           1088
                                                                                                                                                                                                               1028
                                                                                                                                           592
       652
                                                                                                                                                                                                                                            532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Pax:81-438-52-3986) NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB, HRI and Biotechnology Center to.); National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Magatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T. NEDO human cDNA sequencing project Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 4966)
Isogai, T. and Yamamoto, J.
GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAG 692
                                                                       GGGCCTACCATCTCGTATGCCTGGACCCCAGAGCTGGAGAAGGCCTCCCGAGGGCAAGTGGA
                                                                                                                                           GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                            AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAGATCATCCTGTGCGACACCTGCCCGA 1087
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDGYETDHQDYCEVCQQGGEIILCDTCPRAYHLVCLDPELEKAPEGKWSCPHCEKEGI
QWEPKDDDDEEEEGGCEEEEDDHWEFCRVCKDGGELLCCDACESSYHLHCLNPPLPEI
PNGEWLCPRCTCPPLKGKVQRILHWRWTEPDAPFNVGLEGEPESYHLHCLNPPLPEI
REFFVKWAGLSYWHCSWYKELQLELYHTVMYRNYQRKNDMBEPPFDYSGDEDGKSE
KRKNKDPLYAKMEEF FYRYGIKPEWMMIHRILNHSFDKKGDVHYLIKWKDLPYDQCTW
BIDDID PYYDNLKQAYWGHRELMLGBDTGLFKRLLKKGKKLNDCKQEKPPDTPIVDP
TVKFDXQPWYIDSTGGTLHPYQLEGLNWLRFSWAAGTDTILADDMGLGKTVQTIVFLY
SLYKEGHSKGFYLVSAPLSTIINWEREFEMMAADFYVVTYTGDKESRSYLVERNEFSFE
DNAIRSGKKVFRMKKEVQIKFHVLLTSYELITIDQAILGSIEMACLVVDEAHRLKNNQ
SKFFRUNNSYKLDYKLLLTGTPLQNNLEEEFHLLNFLTPERFWLLEGFLEEFADISKE
SKFFRUNNSYKLDYKLLLTGTPLQNNLEEEFHLLNFLTPERFWLLEGFLEEFADISKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKDKKEKKAKRKKKDEDEDDNDDGCLKEPKSSGQLMAEWGLDDVDYLFSEEDYHTLTN
YKAFSGPLRPLI AKKNPKI PMSKMMTVLGKKWREPSANNPFKESAAAAAAAVAAAVE
TVT1SPELAVSSPQVPQPVPI KAKKTKEGKGPGVRKKI KGSKDGKKKGKKTAGLKF
RFGGISNKRKKKGSSSEEDEREESDFDSASIHSASVRSECSAALGKKSKRRKKKRIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSLPKKKKPKKLKENKCKGKRKKKEGSNDELSENEEDLEEKSESEGSDYSPNKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSSCRERRCFLRRRRSWTSWS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQIKKLHDLLGPHMLRRLKADVFKNMPAKTELIVRVELSQMQKKYYKFILTRNFEALN
SKGGGNQVSLLNIMMDLKKCCNHPYLFPVAAVEAPVLPNGSYDGSSLVKSSGKLMLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atwarktpghrsqgspwksrpfqppwiewrvrtstraqparrepersgqrrrrpppp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGAQQFCF1LSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQTKWKPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMLKKLRDEGHRVLIFSQMTKMLDLLEDFLEYEGYKYERIDGGITGGLRQEAIDRFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MRGPVGTEEELPRLFAEEMENEDEMSEEEDGGLEAFDDFFPVEP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAC86802.1"
/db_xref="GI:34533780"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="BRAWH3"
note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="brain"
clone_lib="BRAWH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mol_type="mRNA"
(db_xref="taxon:9606"
(clone="BRAWH3032571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             4.2%;
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                                                                                                                                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 9; Length 4966; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                             60; Indels
                                                                                                                                                                                                                                                                                                                                                <u>.</u>
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SOURCE
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AF425231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           닭
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-SEP-2001) Oncology, Chile Philadelphia, 3615 Civic Center Blvd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 9646)
Thompson, P.M., Gotoh
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thompson, P.M., Gotoh, T., White, P.S. and Brodeur, G.M. CHD5, a New Member of the Chromodomain Gene Family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preferentially Expressed in the Nervous System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF425231.1 GI:19773959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF425231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 9646)
                                                                                                                                                                                                 GDGYETDHQDYCEVCQQGGEIILCDTCPRAYHLVCLDPELEKAPEGKWSCPHCEKEGI
QWEPKDDDDBEEEGGCEEEDDHMEFCRVCKIOGGELLCCDACESSYHLHCLINFPLEBI
PMGBWLCPRCTCPPLKGKVORILHWRHTERPAPEMVGLIAGPDVEBSELPPKPLEGIFE
REFYKWAGLSYMHCSWYKELQLELYHTVMYRNYQRKNDMDEPPPDYGSGDEDGKSE
REKNIKDPLYAKMEERRYRYGIKPEMMMIHRILMHSFDKKGDUHYLIKWKDLPYDQCTW
EIDDID I PYYDNLKQAYWGHRELMLGEDFTRLFKEHLKKGKKLDDDKQEKPDTFI VDP
TVKFDKQPWYLDSTGGTLHPYQDLEGLIMWLRFSWAQGTDTILADEMGLGKTVQTI VFLY
SLYKDGKSWYTDSTGGTLHPYQDLEGLIMWLRFSWAQGTDTILADEMGLGKTVQTI VFLY
SLYKDGKSKYVFRMKKEVQIKFFWLLTSGLITIDGAIGS IEWACLVVDEAHRLKONQ
SKFFRVLNSYKIDYKLLTGTPLQNNLEELFHLLNFLTPERFNNLEGFLEBFADISKE
DNAIRSGKKVFRMKKEVQIKFHVLLTSYELITIDGAIGSSLVKSSGKLMLLQ
KMLKKLRDEGHRVLIFSQMTKMLDLLEDFLEYBGYKYBBIDGSITGGLRGBAIDRENA
SKGGGNQVSLLNIMMDLKKCCNHPYLFPVAAVEAPVLPNGS YDGSSLVKSGGKLMLLQ
KMLKKLRDEGHRVLIFSQMTKMLDLLEDFLEYBGYKYBBIDGGITGGLRGBAIDRENA
PGAQQFCFLLSTRAGGINLATADTYII YBDSDWNFHNDIQAFSRAHRLGQNKKVMIY
PGAQQFCFLLSTRAGGINLATADTYII YBDSDWNFHNDIQAFSRAHRLGQNKKVMIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKAFSQFLRPLIAKKNPKIPMSKMMTVLGAKWREFSANNPFKGSSAAAAAAAVAAAVE
TVTISPPLAVSPPQVPQPVPIRKAKTKEGKGPGVRKKIKGSKDGKKKGKGKKKTAGLKF
RFGGISNKRKKKGSSSEEDEREESDFDSASIHSASVRSECSAALGKKSKRRKKKRIDD
                        EKILIRHHYEQQQEDLARNIGKGKRIRKQVNYNDASQEDQEWQDELSDNQSEYSIGSED
EDEDFEERPEGQSGRRQSRRQLKSDRDKPLPPLLARVGGNIEVLGFNARQRKAFLNAI
MRWGMPPQDAFNSHWLVRDLRGKSEKEFRAYVSLFWRHLCEPGADGAETFADGVPREG
                                                                                                                RFVTRASVEERITQVAKRKMMLTHLVVRPGLGSKSGSMTKQELDDILKFGTEELFKDD
VEGMMSQGQRPVTPIPDVQSSKGGNLAASAKKKHGSTPPGDNKDVEDSSVIHYDDAAI
SKLLDRNQDATDDTELQNMNEYLSSFKVAQYVVREEDGVEEVEREIIKQEENVDPDYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSLPKKKKPKKLKENKCKGKRKKKEGSNDELSENEEDLEEKSESEGSDYSPNKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="chromodomain helicase DNA binding
/protein_id="AAL98962.1"
/db_xref="GI:19773960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CHD5"
101. .5965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
JSRQHVLTRIGVMSLVRKKVQEFEHVNGKYSTPDLIPEGPEGKKSGEVISSDPNTPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKDKKEKKAKRKKKDEDEDDNDDGCLKEPKSSGQLMAEWGLDDVDYLFSEEDYHTLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MRGPVGTEEELPRLFAEEMENEDEMSEEEDGGLEAFDDFFPVEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   map="1p36.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="CHD5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9606"
chromosome="1"
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lvd., Philadelphia, PA 19104-4318,
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COMMENT
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ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    JOURNAL
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusins, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 AGGACGAGTGTGCCGTGTCGGGGACGGCGGGGAGCTCATCTGCTGACGGCTGCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC058578 6438 bp mRNA linear ROD 30 Mus musculus chromodomain helicase DNA binding protein 4, (CDNA clone MGC:68269 IMAGE:6489649), complete cds.
                            cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                  Submitted (22-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6438)
DNA Sequencing by: Nation Sequencing Center (NISC),
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BC058578.1 GI:35193270
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                                                                                                                      Tissue Procurement: The Cepko Laboratory
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SKESLAGNKPANAVLHKVLNQLEELLSDMKADVTRLPSMLSRIPPVAARLQMSERSIL
SRLTNRAGDPTIQQGAFGSSQMYSNNFGPNFRGPGPGGIVNYNQMPLGPYVTDI"
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Pred. No. 0.012;
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Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Alle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Districh,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                          YTPGKKKKKIG JENGANGA JAKUPKI JAKUPKI JAKUPKI JAKUPKI JAKUPKI JENGANG JI DHVF SEEDVETTITNYKA FSQEVRP LI AAKUPKI AVSKMMVLJAKWREE STAULEDWGME JI DHVF SEEDVETTITNYKA FSQEVRP LI AAKUPKI AVSKMMVLJAKWREE STAURE FKGSSGAS VAAAAAAVAVVESMVTATEVA PP PP PEVEVP I KKATKEGKGPNARKEKKGS PR VPDA KKEKEKKEKKEKEE STAUGSTENDILDVESD FDDAS I NSYSVSDOST SERSK KKEKEKEES SEEDDLDVESD FDDAS I NSYSVSDOST SERSK SKKEKETAKKKKKKEGEES VTA VDGY ETDHODYCEVCQQGGEI I LCDTCPRAYHWCLDP DMEKAP BEGKMSC PHCEKEG JQ MERAEDNES GESEI JEEVGD PEEDDHHME FCR VCKD GGELLCCDTCPSS YHIKCLUP LJPE JP JOB JERF VRHCKWYSLELH LWKWGQPPS PT PVRPEPDAD PITES PKELEGR PERQP PVKQGMS YHICSWSELQLELH CQVMFRN YQRKUNMDE PESGE PEGDEKSKRKINKD PK PAMEER PYRYG I KPEMMI HR I LUHS VDKKGHYYLI KKMDL PY DASAMESED VEI QOYDL FKASWERLIKGESER PGKKL KVVLRKLER PET PTVD PTVKYERQ PEYLDATGGTILP YQMEGLUMLRESWAQGTDT I LADBMGLKTYQTA YELY SLYSEGHS KOP LVSA PLST I INWERE FEMMA PDMY VT YVGDKUSRA I I RETESF FEDNAL RGGENG SKOP LVSA PLST I INWERE FEMMA PDMY VT YVGDKUSRA I I RETESF FEDNAL RGGENG SKOP LVSA PLST I INWERE FEMMA PDMY VT YVGDKUSRA I I RETESF FENALAR GGGON CHALLAR FALAND FKUNPSKTELI YR VELS FEMMA PLANT LIGHT YN SELL TI DASALI AGSKKARSIKKKARSIKKKARSVKFHVLLIT YS ELL TI DVAA I LG SI DWACLI VDEAHRLKONGSKFFR VLNGYSLQHKLLLTGTP LQNNLEEL FHLLNPLTP ER FHILLGFLES FAD I AKEDQ I KKLHDMLGFRAFILO FKOCHNPKTE FOLAMAP SKYGSMS KQELDSI TOMROGEA I DRENA PGAQQFC FLLSTRAGELGI KKCCMHYTL FOLAMAP SKYGSMS KQELDSI DET SKYTTS PAGAGDEDD PERSEAP RAPSKYGSMS KQELDSI DET SKYGSMS KQELDSI DET SKYTOSMS KQELDD PERSEAP RAPSKYGSMS KQELDSI DRENG SKYTTS PAGAGDEDD PERSEAP RAPSKYGLANDKOK PKONSOL SKYGSMS KYTTS PAGAGDEDD PERSEAP RAPSKYGNKS LEFKALVS KAGANG KAS SKYTTS PAGAGDEDD PERSEAP RAPSKYGLANDKOK PKONSOL SKYGSMS KAGANG KAS SKYTTS PAGAGDED PODA FTTQW LTRKKYCH KAGANG KAS SKYTTS PAGAGDED PAGAGNA PAGAGD KAGANG KAS SKYTTS PAGAGDED PAGAGNA PAGAGD KAGANG KAS SKYTTS PAGAGDED PAGAGNA PAGAGD KAGANG KAS SKYTTS PAGAGD PAGAGNA PAGAGNA PAGAGNA PAGAGD KAGANG KAS SKYTTS PAGAGD PAGAGNA PAGAG
IRKKVQEFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQPNTPAPVPP
AEDGIKIEENSLKEEBSTEGEKEVKSTAPEATVECAQPPAPATATAPATATAPEDDKA
PAEPPEGEEKVEKAEVKERTBEPMETEAKGTTEVEKVEEKSAVDLTPIVVEDKEEKKE
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EAETPKLKKKKPKKPRDPKIPKSKRQKKELGDSSGEGPEFVEEEEEVALRSDSEGSD
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/tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="chromodomain helicase DNA binding protein
/protein_id="AAHS8578.1"
/db_xref="GI:35193271"
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/db_xref="LocusID:107932"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Debrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Debrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Garad, Pierre, N., Hagos, B., Horton, L., Hune, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lindblad-Toh, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacConald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Worbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuubck, R., Stange-Thomann, N., Stolanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travers, M., Traylio, J., Ye, W. J., Voung, G., Zainou, J., Zembek, L., Zimmer, A. and Zody, M.
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 67573)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArtellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-MAY-2002) Whitehead Institute/MIT Center
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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KEYWORDS SOURCE ORGANISM

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Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Robupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zembek,L., Zimmer,A. and Zody,M. Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 15, 2002 this sequence version replaced gi:21206372. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Direct Submission

http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu

NOTE: This record contains 84 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone be preserved. will be sequenced to completion. In the event the record is updated, the accession number will

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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Query Match
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Matches 89; Conser
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AC134529 173909 bp DNA linear HTG 05-MAR-2003 MUS musculus chromosome UNK clone RP24-503A2, WORKING DRAFT SEQUENCE, 5 unordered pieces.
AC134529
                                                                                                                                                                                                                                                                                                                                                        43396
43496
44182
44282
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                          4.18;
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44181:
44281:
45002:
                                                                                                                                                                                                                                                                                                                                                     gap of contig gap of contig
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                                                                                                                                                                                                                                                                                            Score 63.2; I
Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                                                          No. 0.019;
                                                                                                                                                                                                                                                                                                                                                     100 bp
of 686
100 bp
of 721
                                                                                                                                                                                                                                                                                                                                                      bp in length
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                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                         Length 67573;
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                   592
                                                                                                                                                                                                                                      12452
                                                                                                                                                                                                                                                                                            0
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Parkway, St. Louis, MO 63108, USA

(bases 1 to 173909)

McPhorson, J.D. and Waterston, R.H.

Direct Submission

Direct Submission

Sequencing Center, 4444 Forest

Parkway, St. Louis, MO 63108, USA

On Mar 5, 2003 this sequence version replaced gi:28626883. 2 (bases 1 to 173909)
McPherson, J.D. and Waterston, R.H.
Direct Submission The sequence of Mus musculus clone Unpublished Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 17399)
McPherson,J.D. and Waterston,R.H. Mus musculus AC134529.3 GI:28850175 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Mus musculus (house mouse) Submitted (27-SEP-2002) Genome Sequencing Center, 4444 Forest Park Park

Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175455 bases at least Q40
Consensus quality: 176221 bases at least Q30
Consensus quality: 176527 bases at least Q30 Center: Washington University Genome Center code: WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml Center project name: M_BB0503A02 Project Information Sequencing Center

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RESULT 53
BV089378/c
                                                                                                                               COMMENT
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                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                  VERSION
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                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 89;
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Best Local
                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 GTGCTCCAGCTG 664
                                                                                                                                            Usuka, J., Liao, G., Cheng, J., McPherson, J.D., Foernzler, D. Mus musculus SNPs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                               tagged site.
BV089378
BV089378.1 GI:37666857
                                                   Contact: Jonathan Usuka
Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
3431 Hillyiew Ave, Mailstop S3-1, Palo Alto, CA (
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 572)
                                                                                                                                                                                                                                                                                                                                                                                    BV089378 572 bp I
RPAMMSEQ0001274 Roche Palo Alto Mus
Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCTACCACATCCACTGCCTGAACCCCCCCGCTGCCAGAGATCCCCAAACGGCGAATGGCT 12928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GECCTTCCACCTGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG
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be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTCCCCGCTG 12940
                                                                                                                                                                                                                                                                                          musculus (house mouse)
                                     6508555807
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93711. .173909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig28" 38628. .93610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP24-503A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
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1. .173909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1200: contig of 1200 bp in length
6880: gap of unknown length
6880: contig of 5580 bp in length
6980: gap of unknown length
38527: contig of 31547 bp in length
38627: gap of unknown length
93610: contig of 54983 bp in length
93710: gap of unknown length
173909: contig of 80199 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.2; DB:
Pred. No. 0.016;
                                                                                                                                                                                Nguyen, A., Bach, C., Puech, A., and Peltz, G.
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                                                       Palo Alto, CA 94024, USA
                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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                                                                                                                                                                                                                                                                                                                                                                                       musculus
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                                                                                                                                                                                                                                                                                                                                                                                                         linear
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AC097256/c
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Best Local
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                                                RS Muzny, D. Marie., Metker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Bardaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Carden, R., Canter, K., Cavazos, I., Ceasar, H., Center, A., Center, A., Center, A., Center, A., Cracker, A., Carden, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cardenas, V., Carter, K., Carder, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cardenas, V., Chen, Z., Chu, J., De, Anda, C., Dederich, D., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgar, H., Dugan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C., M., Gaber, A., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Handlı, C., Hamilton, C., Hamilton, K., Gill, R., Garcia, A., Garner, T., Garza, M., Guevara, W., Ghregeorgis, E., Geer, K., Haldun, S.L., Hodgson, A., Hogson, A., Hogson, A., Hogeson, A., Johnson, R., Jolivet, A., Karjathy, S., Kelly, S., Khan, Z., King, L., Kus, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer B: No primer submitted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
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AC097256.6 GI:30521113
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Rattus norvegicus clone CH230
                               Milosavljevic, A., Miner, G., Minja, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ***, 5 unordered pieces.
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/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ, -129/Sv, AKR/J, B10.D2-H2/oSnJ,
BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.~"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10090"
/map="10-9361-9932_CAAA01111727.1.1.11206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol type="genomic DNA"
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Pred. No. 0.05
0; Mismatches
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CH230-172E6,
a,E., Montemayor,J., Moore,S., Munidasa,M., Murphy,M., Nair,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
,.05;
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6, ***
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SEQUENCING
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IN PROGRESS
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23100986.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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K., Pascernak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
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Direct Submission
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                                                                    as soon as it is available and the accession number will be preserved.
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------ Project Information
Center project name: GRRK
Center clone name: GRRK
Center clone name: GRRK
Center clone name: GR20-172E6
------ Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 21293 bases at least Q40
Consensus quality: 215360 bases at least Q20
Consensus quality: 21739 bases at least Q20
Betimated insert size: 225359; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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23011: contig of 23011 bp in length
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COMMENT

REFERENCE TITLE JOURNAL

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TITLE JOURNAL REFERENCE

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Matches 119;
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RS Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Conterl, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davils, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davils, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Eggan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Gardy, M., Gerner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevra, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Hernandez, J., Hollins, B., Howels, S., Hladun, S.L., Hodgson, A., Hernandez, J., Jackson, A., Jackson, A., Jackson, A., Jackson, L., Jackson, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Jackson, A., Johnson, R., Johnson, R., Jolivet, A.,
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP
Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-28C23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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/db_xref="taxon:10116"
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244670: contig of 221559 bp in length
244770: gap of unknown length
245826: contig of 1056 bp in length
245826: gap of unknown length
247145: contig of 1219 bp in length
247145: gap of unknown length
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248835: contig of 1590
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WORKING DRAFT SEQUENCE.
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Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhwaa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidas, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherrer, S., Scott, G., Shateman, S., Shen, H., Sned, A., Sodergren, B., Song, X.-Z., Sortle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Wang, Q., Wang, S., Warren, J., Warren, J., Warren, J., Walker, B., Wang, J., Wang, S., Wallson, R., Willson, R., Willson, H., Wooden, H., Worley, K., Williams, G., Willson, R., Willson, S., Thomas, S., Tong, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Mang, O., Smith, H.D., Smith, H.O., Mang, O., Smith, D.R., Holt, R.A., Smith, D.R., Holt, R.A., Smith, D.R., Holt, R.A., Smith, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23265433.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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3 (bases 1 to 273874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Sequencing Consortium.
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Kowis,C., Kraft,C.L., Lebow,H., Levan,J.,
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                                                                                                                                                                                                               Center project name: GXLZ
Center clone name: CH230-28C23
Center clone name: CH230-28C23
Center clone name: CH230-28C23
Assembly program: Phrap; version 0.990329
Consensus quality: 230595 bases at least Q40
Consensus quality: 230595 bases at least Q30
Consensus quality: 232954 bases at least Q20
Consensus quality: 234439 bases at least Q20
Estimated insert size: 234885; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                       Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

COMMENT

REFERENCE AUTHORS

JOURNAL TITLE

> Direct Submission Harrison, E

Submitted (09-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                    218721
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 121375)
                                                                                 Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                     complete sequence BX004850
                                                                                                                                                                                                          BX004850 121375 bp DNA linear VRT 10-JUN-200 Zebrafish DNA sequence from clone CH211-51M24 in linkage group 19,
                                                                                                                                                  BX004850.11 GI:48596641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTTCCACCTGGCCTGCCCTCCCGCTCCGGGAGATCCCCAGTGGGAACCTTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGGGGGGCTCATCTGCTGTGACGGCTGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCCCTCGATGCACGGTAAGTAGAACCTCATCCTCACAGCGCCCACCATCCAAGCGCCA 21878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTACTGCCGAGTGTGCAAGGACGGCGGGGGGGCTCCTGTGCTGTGACGCCTGCATCTC 218660
                                                                                                                                                                                                                                                                                                                                    CCTTTCAGCCATTTCTGAGGCCGCGCAGCTCTTCC 218815
                                                                                                                                                                                                                                                                                                                                                                             GCCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by the finished sequence as soon as it is available the accession number will be preserved.

1 273874: contig of 273874 bp in length.
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complement(271364, .272156)
/note="clone_boundary
clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end_sequence:BH340767"
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/note="clone_boundary
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Pred. No. 0.034;
0; Mismatches
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                                             Ostariophysi;
                                                              Vertebrata; Euteleostomi;
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ACCESSION
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CQ541728
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeate; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish puc Subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71538
                                                                                                                                                                                                                                                                                                                                71418
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                                                                                                                                                                                                                                                                                                                                                                                649
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                                                                                                                                  Sequence
CQ541728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-51M24 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute Center code: SC
Eukaryota; Metazoa; .Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                        CQ541728.1 GI:41507992
                                                                                                                                                                                          CQ541728
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGGGCCTATCACATGGTCTGGCTTGGACCCCGACATGGAGAAGGCCCCTGAGGGTACCT 71419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAGGATTACTGTGAGGTCTGCCAGCAGGAGGTGAGATCATTCTCTGTGACACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      creaeeccrrecaecreeccreccrececreececeeeaearcccaereeaeccr
                                                                                                                                                                                                                                                                                                                                GGAGCTGCCCACACTGCGTGAGTGAACCGG 71389
                                                                                                                                                                                                                                                                                                                                                                                GGAGGTGCTCCAGCTGCCTGCAGGCAACAG
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                                                                                                                                                           11363 from Patent
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/db_xref="taxon:7955"
/clone="CH211-51M24"
/clone_lib="CHORI-211"
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                                                                                                                                                                                                                                                                                                                                                                                678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seelig, H.P. and Renz, M.
DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
PATENT: WO 9628547-A 1 19-SEP-1996;
PRIVATES INST FUER IMMUNOLOGIE (DE)
Other publication DE 19509279 960515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCGGCTGTAAACAGCTCTGTGTTTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTA
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                                                                                                                                                                                                                                                /translation="AGGLGSPSPCSAGSEEEDMDALLMNSLPPPHPENEEDPEDLSE
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CRVCLDFDMEKAPEGKWSCPHCEKEGIQMEAKEDNSEGEELIEBVGGGLEEEDDHHMSF
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DMYTVTYTYCGOKDSRAIIRENEFSEDNAIRGGKKASRNKEASSVKFHVLLITSYELHII
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DMYTVOTTYCGOKDSRAIIRENEFSEDNAIRGKGANSRNKEASSVKFHVLLTSYELHII
DMYTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGTUTGANGT
                           APKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGHRVLIPSQMTKMLDLLEDPLEHE
GYKYERIDGGITGNMRQEAIDRFNAPGAQQFCPLLSTRAGGLGINLATADTVIIYDSD
WNPHNDIQAPSRAHHIGQNKKVMIYRVTRASVBERITQVAKKKMLTHLVVRPGLGS
                                                                                                                                              DMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHKLLLTGTPLQNNLEELFHL
LNFLTPERFHNLEGFLEEFADIAKEDQIKKLHDMLGPHMLRRLKADVFKNMPSKTELI
VRVELSPMQKKYYKYILTRNFEALNARGGGNQVSLLNVVMDLKKCCNHFYLFPVAAME
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/db_xref="taxon:9606"
KTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGEDSSVIHYDDKAIERLLDRNQD
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/proteIn_id="CAA03424.1"
/db_xref="GI:3712831"
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AUTHORS
TITLE
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KEYWORDS
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Sequence 1 1
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Seelig, H.P. and Renz, M.
Dermatomyositis-specific auto-antigen
Patent: US 6440679-A 1 27-AUG-2002;
Location/Qualifiers
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Sequence 1 from patent US 6440679
AR224019
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              AR269336.1
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                                                                                                                                                                                                  GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGA 651
                                                                                                                                                                                                                                                               AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                                                                                                                       GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG
                                                                                                                                                                     GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
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AFTTOMLVRDLÆKSEKEFKAYVSLFWEHLCEPGADGAETFADGVPREGLSRGHVLTR
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PEGEEKVEKAEVKETEEPMETEPKGAADVEKVEEKSAIDLTPIVVEDKEEKKEEEEK
KEVMLQNGETPKOLNIDEKQKKNIKQRFWINIADGGFTELHSLMQNEERAATVTKKTYE
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
/mol_type="genomic
                                          from patent
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Pred. No. 0.12;
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Seelig,H.P. and Renz,M.
Dermatomyositis-specific auto-antigen
Patent: US 6339517-A 1 11-DEC-2001;
Location/Qualifiers
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Seelig, H.P. and Renz, M.
Dermatomyositis-specific auto-antigen
Patent: US 6500923-A 1 31-DEC-2002;
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/mol_type="genomic |
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Patent: W
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Sequence 2747 from Patent W00194629.
AX332238
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Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                              Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 02068579-A 8343 06-SEP-2002; PE Corporation (NY) (NG)
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatea; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA 1317
                                 GGGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA 651
                                                                   AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCCC
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                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The major dermatomyositis-specific Mi-2 autoantigen is a presumed helicase involved in transcriptional activation Arthritis Rheum. 38 (10), 1389-1399 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 6417) Seelig,H.P., Moosbrugger,I., Ehrfeld,H., Fink,T., Renz,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              helicase; Mi-2 gene;
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSMI2218 6417 bp mRNA H. sapiens mRNA for 218kD Mi-2 protein.
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KGSSGASVAAAAAAVAVVESNVTATEVAF PPPPWEVPIRKAKTKEGKGENARRKPKG
SPRVPDAKKPKKVAPKLXIKLGFGSKRKRASSEDDDLDVESDFDDASINSVSVSSG
STSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHODYCEVCQQGGEIILCDTCPRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="masglgspspcsagseeedmdallunslppppppeedleedbls
etetpklkkkkkpkkprdpkipkskrokkermllcrqlgdssgegpefveeeeevalr
sdsegsdytpgkkkkkkklgfkkekkskskrkeeeedddddskepkssaqlledwgm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Mi-2 protein"
/protein id="CAA60384.1"
/db_xref="COA:01696"
/db_xref="GOA:Q1839"
/db_xref="Swiss-Prot:Q14839"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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|...6417
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9, D-76133 Karlsruhe, FRO
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RESULT 66
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AR338834
  KEYWORDS
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AR338834
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Trang,Y.T., Zhou,P. and Drmanac,R.T.
Nucleic acids and polypeptides
Patent: US 6569662-A 3.25 27-MAY-2003;
                                                                                                                                         BC038596
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                                                                          3C038596 6584 bp mRNA linear PRI 0. Homo sapiens chromodomain helicase DNA binding protein 4, (CDNA clone MGC:46187 IMAGE:5528023), complete cds.
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                                                                                                                                                                                                                                                                                                                                    GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                                                                                                                                                                                                                                                                                                                                          GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCTTCCACCTGGCCTGTCCCCTCCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                             GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1482
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TPAPVPPARDGIKIERNSLKERESIEGEKEVKSTAPETAIECTQAPAPASEDEKVVVE
PPEGEKVVPPAKDGIKIERNSLKERESIEGEKEVKSTAPETAIECTQAPAPASEDEKVVEE
PPEGEKVEKALDLIPFVQDKEEKKEEEE
PPEGEKKVEKALDLIPFVADKREKKEEEE
KKEVMLQNGETPKOLNDEKQKKNIKQREMENIADGETELHSLMQNEERAATVTKKTY
EIWHRRHDYWLLAGIINIGYARMQDIQNDPRYAIINEPFKGEMNRGNFLEIKNKFUKTY
RFKLLEQALVIEEQLRRAAYLNMSEDPSHPSMALNTRFAEVECLAESHQHLSKESMAG
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1. .6475
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MEDLINE
PUBMED
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TITLE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,

Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 78 Row: o Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nc
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                              /clone="MGC:46187 IMAGE:5528023"
/tissue type="Skin, melanotic melanoma.
/clone_lib="NIH_MGC_72"
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/db_xref="taxon:9606"
                                                         L. .6584
                                                                                                                                                                                                                                                                                                          L. .6584
                                                                                   note="Vector:
                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                               lab host="DH10B"
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CLDPDWEKAPECKWSCPHCEKEGIQWEAAKEDNSEGETLEEVQGDLEEEDDHHMEFCR
VCKDGGELLCCDTCPSSYHIHCLNPPLPEIPNGEMLCPRCTCPALKGKVQKILIIKKWG
QPSSPTPVPRPDAD PNTTSSPKPLEGR PERQPFVKWQCWSYMHCSWVSELQLELHCQV
MFRNYQRKUDWDEPPSGDPEGGDEEKSRKRKNKDPKPAEWEERFYRYGIKPEWMAIHRI
LNHS VDKKGHVHYLIKWRDLPYDQASWESEDVEIQYDLFKQS YWHRELMGEEGRP
GKKLKKVKLRKLER PETTTYDPTVKYERQPEYLDATGCTLHPYQMEGLIMWLR FSWAQ
GTDTILADEMGLGKTVQTAVPLYSLYKEGHSKGPPLYSAPLSTIINWEREFEMMAPDM
GTDTILADEMGLGKTVQTAVPLYSLYKEGHSKGPPLYSAPLSTIINWEREFEMMAPDM
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PHNDIQAFSRAHRIGGGNAVVVREEEMGEEEEVEREIIKQESVDFDWEKLLRHHYE
QQCDELLARNLGKGKIRKGCHNMIYRFVTRASVEERITOWLKKCMMLTHLVVR PGLGSKT
GSMSKGBLDDILKFGTEELFANDGTDFDRASEAFRRESESVIKTANUGDFLPLLAFVGENI
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DGGFTFELHSLMONERBAATVYKGTYETHERBHDYMLLAGIILAGIILAGIINDEKAANDDFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PHD; Region: PHD-finger. PHD folds into an interleaved type of Zn-finger chelating 2 Zn ions in a similar manner to that of the RING and FYVE domains" /db_xref="CDD:pfam00628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CHD4"
/note="PHD; Region: PHD-finger. PHD folds into an interleaved type of Zn-finger chelating 2 Zn ions in similar manner to that of the RING and FYVE domains"
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ILNEFFKGEWNRGNFLEIKNKFLARRFKLLEQALVIEBQLRRAAYLNWSEDPSHPSMA
LNTRFAEVECLAESHQHLSKESWAGNKFANAVLHKVLKQLEELLSDMKADVTRLPATI
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DHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVSKMMVLGAKWREFSTNNPFKGS
SGASVAAAAAAVAVVESMVTATEVAPPPPVEVPIRKAKTKEGKGPNARRKPKGSPR
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2017. .2181
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                                                                                                                                                                                                                                                                                                                                   domain"
                                                                                                                                                                                                                                                                                                                                                        /gene="CHD4"
/note="CHROMO; Region: Chromatin organization modifier
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l63. .5976
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REFERENCE
AUTHORS
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ORGANISM
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AL589792
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VERSION
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Matches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 12% of reads
Sequencing vector: plasmid; L08752; 87% of reads
Chemistry: Dye-terminator ABI; 14% of reads
Chemistry: Dye-terminator Big Dye; 60% of reads
Chemistry: Dye-primer-ameraham; 24% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 131458 bases at least Q40
Consensus quality: 131709 bases at least Q30
Consensus quality: 131965 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1382 GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1262 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL589792 DNA linear HTG 10-JI Homo sapiens chromosome 1 clone RP5-889P23 map p36.21-36.33,
                                                                                                                                                                                                                                                                                                                               Insert size: 132292; sum-of-contigs
Insert size: 132129; 14.2% error; agarose-fp
Quality coverage: 11.37x in Q20 bases; sum-oc
coverage: 11.69x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: dJ889P23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                          AL Submitted (20-0UL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone request8: clonerequest@sanger.ac.uk

On Jul 22, 2000 this sequence version replaced gi:9368784.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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                       The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lt6518 bp DNA linear PR Human DNA sequence from clone RP1-120G22 on chromosome 1p36.21-36.33, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                feature key.
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Location/Qualifiers
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/clone="RP5-889P23"
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/chromosome="1"
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Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP1-120G22 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2 was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

1. .166518 ocation/Qualifiers

/note="match: GSS: Em:AQ213363"
complement(41123. .41505)
/note="match: GSS: Em:AQ133445" /note="Single clone region. short insert library only" complement (57981. .58764) /note="match: GSS: Em:AF158011" /note="match: 94030..94434 /note="match: 88780. .89285 /note="match: 87339. .87808 complement (86963. complement (85942. complement (79935. complement (79556. /note="match: GSS: complement(79470... complement (74554. /note="Single clone region. short insert library only"
68250. .68620 64797. complement (60582. complement (41087. .41505) /note="match: GSS: 18389...18823 /note="match: GSS: Em:AQ239786" 10012. .10541 /note="match: GSS: Em:AQ716455" 8816. .9229 /note="match: /note="match: STS: Em:G21080" 45297. .45591 /note="match: 25588. .26045 /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="1" /organism="Homo sapiens" /mol_type="genomic DNA" note="match: STS: Em:HSA052WG1" note="match: note="match: STS: Em:AF191963" note="match: STS: Em:G16281" note="match: GSS: Em:AQ695221" note="match: GSS: Em:AF046498" note="match: 25694. /map="p36.21-36.33" /clone="RP1-120G22" note="match: clone_lib="RPCI-1" .70622 .64841 GSS: GSS: GSS: STS: GSS: Em:AQ097494" GSS: Em:AQ214655" GSS: GSS: Em:AQ541496" .86372) .80319 .79740) .61043) Em: AQ678815" Em: B89150' Em: AQ698012" Em:G22706" Em: AQ097224" Em: AQ121434" Em: AQ191756" 87322) Em: AQ270793"

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/note="match: GSS: Em:AQ489599"
complement(113100. .113712)
/note="match: GSS: Em:AQ477048"
complement(113175. .113715)
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94054. .94464
94054. .94464
/note="match: GSS: Em:AQ010380"
join(112106. .112211, 116809. .116933,123047. .123132)
/note="match: GSS: Em:AQ634365"
complement(join(112121. .112215,116809. .116936))
/note="match: GSS: Em:AQ202845"
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complement(124491. .124832)
/note="match: STS: Em:G06939"
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/note="match: GSS: Em:AQ779080"
123142. .123248
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116809. .116936
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join(11609. 11693),123047. 123119)
/note="match: GSS: Em:AQ732842"
116809. 116941
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123192. .123356
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|001n(116840. .116933,123047 .123191)
|roote="match: STS: Em:G13224 Em:G13474"
|21507 .121762
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113710. .114090
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join(112145. .112211,116809. .116936)
note="match: GSS: Em:AQ634370"
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Matches 103;
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1 (bases 1 to 1591)

Ge,Q., Nilasena,D.S., O'Brien,C.A., Frank,M.B. and Targoff,I.N. Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2 autoantigen

J. Clin. Invest. 96 (4), 1730-1737 (1995)
                                                                                                                                                                                                                                                      Submitted (06-APR-1994) M. Bart Frank, Foundation, Arthritis and Immunology P. Oklahoma City, OK 73104, USA Location/Qualifiers
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Human Mi-2 autoantigen
U08379
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Targoff, I. N. and Ge, Q.
Antigens associated with polymyositis and Patent: US 6610823-A 1 26-AUG-2003;
Location/Qualifiers
1. .1053
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                                                        <1. .>1591
/note="Northern blot with this cDNA a single band in 7.5 kb region"
                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                        /cell_type="thymocyte"
/tissue_type="thymus"
/clone_Tib="thymocyte and
(Clontech)"
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/mol_type="mRNA"
                                          evidence=experimental
                                                                                                                                                                           clone="C4"
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          partial cDNA encodes an antigenic region
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Pred. No. 0.17;
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Sequence 23239 from Pat
CQ491372
CQ491372.1 GI:41456991
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Millennium Predictive Medicine, Inc. (U
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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23239 from Patent WO0160860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DN/
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532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                              AX924076
Sequence 30 from Patent
AX924076
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Sequence 29 from Patent
AX924075
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                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                    Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                Conservative
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                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human
Genome Research Institute, National Institutes of Health, 49
Convent Drive, Bethesda, MD 20892-4442, USA
Location/Qualifiers
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1 (bases 1 to 6331)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Characterization Sci. U.S.A. 94 (21), 11472-11477 (1997)
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Homo sapiens CHD3 mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGCCCTCACTGTGAGAAGGAGGGGGGGGGGAGGCCCAAGGAGGAAGAAGA 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGGA 706
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EEDDHMEYCRVCKDGGELLCCDACISSYHIHCLNPPLPDIPNGEWLCPRCTCPVLKGR
VQKILHWRWGEPVAVVAPQADGNEDVPPERPLQGRSEREFYVKWGLSYWHCSWAK
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VPDGRKKLTGKKMAPLKIKLGLLGGEPAVAGEEEVDGYETDHQDYCEVCQQGGEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCDTCPRAYHLVCLDPELDRAPEGKWSCPHCEKEGVQWEAKEEEEEYEEEGEEEGEKE
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/chromosome="17"
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LLRHHYEQQOEDLARNLGKGKRVRKQNNYNDAAQEDQDNQSEYSVGSEEEDEDFDERP
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MKSLVKKVQEFEHINGRWSMPELMPDPSADSKRSSRASSPTKTSPTTPEASATNSPCT
MKPATPAPSEKGEGIRTFLEKEEAAENQEEKPEKNSRIGEKEKETEAPAFDPSBAGRREEKFL
EPRKLFLEDENVGDNELERPGFRDEFPANGRREEKFL
EPRKLFLEDENVGDNELERPGFRDEFPANGRREEKFL
EFRKPRFMFNIADGGFTELHTLMQNEERAAISSGKLNEIMHRRHDYMLLAGIVLHGYARW QDIQNDAQFAIINEPFKTEANKGNFLEMKNKFLARRFKLLEQALVIEEQLRAAYLNL SQEPAHPAMALHARFAEABCLAESHQHLSKESLAGNKPANAVLHKVLNQLEELLSDMK ADVTRLPATLSRIPPIAARLQMSERSILSRLASKGTEPHPTPAYPPGPYATPPGYGAA FSAAPVGALAAAGANYSQMPAGSFITAATNGPIHRFFKKVPEIQ"

REFERENCE AUTHORS DEFINITION ACCESSION VERSION RESULT 75 AX924049 LOCUS ORIGIN SOURCE ORIGIN FEATURES KEYWORDS Query Match Best Local Similarity Matches 103; Conserv TITLE Query Match Best Local Similarity Matches 103; JOURNAL 1406 1286 1466 1346 AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC 592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA 651 652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGGA 706 532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC Sequence 3 AX924049 Al-Mahmood, S., Colin, S. and Schneider, C.
Angiogenesis regulator genes, pharmaceutical preparations
containing same and uses thereof
patent: WO 03080105-A 3 02-OCT-2003; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens (human) Gene Signal (FR) AX924049.1 GI:40217057 AX924049 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGTCCGGGAGATCCCCAGTGGGACCTGGA 651 AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC GCTGCCCTCACTGTGAGAAGGAGGGGGGTCCAGTGGGAGGCCAAGGAGGAAGAAGA 1520 GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591 GCTGCCCTCACTGTGAGAAGGAGGGGGTCCAGTGGGAGGCCAAGGAAGAAGAAGA 1460 GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA Conservative Conservative /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" Location/Qualifiers from Patent WO03080105 3.9%; 58.9%; 3.9%; 0 0 Score 59.8; DB Pred. No. 0.13; Score 59.8; DB Pred. No. 0.13; 6771 bp Mismatches Mismatches BB DNA 72; 6, 72; 9; Length 6771; Length 6331; Indels Indels linear PAT 18-DEC-2003 0 0 Gaps 1345 1405 591 0

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1 (Dases 1 to 6771)

Aubry, F., Mattei, M.G. and Galibert, F.
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U91543
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ERAAI SSGKLNEI WHRRHDYWLLAGI VLHGYARWQDI QNDAQFAI I NEPFKTEANKGN
                                                                                                                                                                                                                                                                                                                               FKNMPAKTELI URVELS PMOKKYYKY I LTRNFEALNSRGGGNOVSLLNI MMDLKKCCN
HPYLF PVAAMES PKLFSGAY EGGALI KSSGKLMILOKMLRKLKEGGHR VL I FSOWTKM
LDLLEDFLDY EGGYKTER I DGGI TGALROEA I DREFNAPGAOOTCFLLSTEAGGGIGJINA
TADTVI I FDSDMNPHND I QAFSRAHR I GOANKVMI YR FVTRAS VEER I TQVAKRKMML
flemknkflarrfklleqalvieeqlrraaylnlsqepahpamalharfaeaeclaes
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151. .6153
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/db_xref="taxon:9606"
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(hZFH) mRNA, complete cds.
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KEYWORDS
SOURCE
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AC135674/c
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                                                                                                                                                      1406
                                                                                                                                                                                                                                                                                                532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                                         HLL136/4 168479 bp DNA linear
Rattus norvegicus clone CH230-368023, WORKING DRAFT
AC135674
                            AC135674.2 GI:25007200
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                   GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                            GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                    GCTGCCCTCACTGTGAGAAGGAGGGGGGTCCAGTGGGAGGCCAAGGAGGAGAAGAAGA 1460
                                                                                                                                                                                                                 GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
                                                                                                                                                                                                                                                                              AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="encodes nuclear targeting sequence"
6744. .6749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="encodes putative zinc-finger helicase formed from alternative splicing; mRNA observed, but no protein yet identified; hZFH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="encodes
2239. .2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(151. .5074,5177. .6153)
                                                                                                                                                                                                                                                                                                                                                                                                                                gene="hZFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="hZFH"
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/gene="hZFH"
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                                                                                                                                                                                                                                                                                                                                                     3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3060
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                     Score 59.8; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear targeting sequence"
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ORGANISM HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE AUTHORS RS Mizny, D. Marie . Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Chacko, J., Chacko, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Cree, A., D'Souza, L., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, K., Harnhoz, J., Harnhoz, J (bases 1 to 168479) Hawes, A., Henderson, N., Hernandez,J.,

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Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meren, E., Marhiney, S., McLeod, M.P., McNeill, T.Z., Menen, E., Murphy, M., Nair, L., Nancervis, C., Nenkon, N., Nouyen, N., Norris, S., Nuackervis, C., Neal, D., Newton, N., Nuyyen, N., Norris, S., Naokelmeh, O., Okwuonu, G., Olarmpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Nuiz, S.J., Riegs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sheity, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Warght, D., Warght, R., Wallson, R., Wleczyk, R., Wooden, H., Worley, K., Waight, D., Warght, R., Wallson, R., Wleczyk, R., Wooden, H., Worley, K., Waight, D., Waight, R., Wallson, R., Wleczyk, R., Wooden, H., Worley, K., Waight, D., Walson, J., Zhou, J., Zhou, J., Zhou, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Smith, D.R., Holt, R.A., Smith, H.O., Weinstobe, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:24181980. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
Submitted (21-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 168479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shotgun sequence only contigs will be indicated in the feature table.
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Direct Submission
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REFERENCE AUTHORS TITLE

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1 (bases 1 to 221787)

Muzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alla Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benz Baldwin, D., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burcell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 168479: contig of 168479 bp in length.
                                                                                                                                                                                                                                                                                             AC119782.5 GI:23670853
HTG; HTGS-PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                            Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; |
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                AC119782
                                                                                                                                                                                                                                                                                                                                                                                                               AC119782 22
Rattus norvegicus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCTACCACTTGCACTGCCTCAACCCGCCGCCGCGGAGATCCCCGAACGGTGAATGGCT 12438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCCAGGAGCCCACCCGTGGAGACCCC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTTCTGTGCTGTGATGCTTGTCCCTC 12498
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/note="clone_boundary
clone_end:T7
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complement(166515...16
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                  221787 bp DNA linear
ne CH230-134M24, WORKING DRAFT
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                                                                                                   Barnstead, M., Benahmed, F.,
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                                                                                                                                                                          Adams, C., Alder, J.,
                                                                                                                                                                                                                                                 Buteleostomi;
; Murinae;
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SEQUENCE.
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Chen, Z., Chu, J.,

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Caveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Soura, M., Debard, S., Debard, S., Devy-Carrolling, P. Bridge, H., Debard, D., Debard, N., Errore, N.
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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SOURCE
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REFERENCE
                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                  POCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         66660 CCCCGCCCGGCCCGGCCCGGCCCGCC 66634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66780 CTCCTACCACTTGCACTGCCTCAACCCGCCGCTGCCGGAGATCCCGAACGGTGAATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 GGCCTTCCACCTGGCCTGTCCCCTCCGGCTCCGGGAGATCCCCAGTGGGACCTGGAG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     653 GTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCG 712
                                   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                    AC097926 246566 bp DN Rattus norvegicus clone CH230-44J16,
                                                                                                                                                               unordered pieces.
AC097926
AC097926.6 GI:30521120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCCAGGAGCCACCCGTGGAGACCCC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCCCGCGCTGTACAGTGAGTGTTACACCTCCTGCCCCGCCCCGCCCCGCCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTTCTGTGCTGTGATGCTTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACGAGTGTGCCGTGTGTCGGGACGCCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the accession number will be preserved.

1 221787: contig of 221787 bp in length.
Location/Qualifiers
(bases 1 to 246566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project Information
Center project name: GWIF
Center clone name: CH230-114M24
Center clone namez CH230-114M24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Phrap; version 0.990329
Consensus quality: 207183 bases at least Q40
Consensus quality: 208452 bases at least Q30
Consensus quality: 208456 bases at least Q30
Estimated insert size: 215794; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wgs_contig"
complement(220394...2
/note="clone_boundary
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site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l_type="genomic DNA
_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59.8; DB 2;
Pred. No. 0.073;
0; Mismatches 92;
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                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                           WORKING DRAFT
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                                                                                                                                                                                                                                           SEQUENCE,
                                                                                                                                                                                                                                              HTG 10-MAY-2003
SEQUENCE, 2
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AUTHORS

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REFERENCE
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JOURNAL
REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                              COMMENT
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23096446.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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FEATURES
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Best Local Similarity
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148705 CCCCGCCCGGCCCGGCCCGGCC 148679
                                                                                                                                                                                                                             148825 CTCCTACCACTTGCACTGCCTCAACCCGCCGCCGCCGGAGATCCCGAACGGTGAATGGCT 148766
                                                                                                                                                                                                                                                                                                                                                 148885 GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTTCTGTGCTGTGATGCTTGTCCCTC 148826
                                                                                                                                                                                                                                                                                       593 GGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                          533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft sequence. It currently

* CONSISTS of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact size of represented as

* runs of N, but the exact size are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                             GTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG
                                                      GCCCCAGGAGCCACCCGTGGAGACCCC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: GFQD

Center clone name: CH230-44J16

Center clone name: CH230-44J16

Center clone name: CH230-44J16

Center Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 234382 bases at least Q40

Consensus quality: 237163 bases at least Q20

Consensus quality: 239522 bases at least Q20

Estimated insert size: 246580; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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complement(243583. .2.
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end_sequence:BH294325"
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site:EcoRI
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236149. .238197
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site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 244590: contig of 244590 bp in length
1 244690: gap of unknown length
1 246566: contig of 1876 bp in length.
Location/Qualifiers
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/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.9%; Score 59.8; DB 2; 55.6%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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SOURCE
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ACCESSION
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KEYWORDS
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CQ720332
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TITLE
                                                      Query Match
Best Local Similarity
                                            Matches
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              653 GTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
                                                                                                                                                                                                                                                                                                                                                                     Sequence
AX655393
                                                                                                                                                                              Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. & Plant genes involved in defense against pathogens Patent: WO 03000898-A 5263 03-JAN-2003; Syngenta Participations AG (CH)
                                                                                                                                                                                                                                                                  Oryza sativa
Oukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6266 from Pate:
CQ720332
CQ720332.1 GI:42281189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 02068579-A 6266 06-SEP-2002; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         AX655393.1 GI:29158207
                                                                                                                                                                                                                                                                                                                                                                                                  AX655393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGCTCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAGATCATCCTGTGCGACACCTGCCCGA
3.8%;
ilarity 65.4%;
Conservative
                                          Conservative 338; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    5263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                            /organism="Oryza sativa"
/mol_type="unassigned DNJ
/db_xref="taxon:4530"
                                                                                                                                                                      Location/Qualifiers
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                                                         3.8%;
11.1%;
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from Patent WO03000898
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                                                       Score 58.8; DB Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59.4; DB Pred. No. 0.16;
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                                                                                                                              DNA"
                                                                     DB 6;
                                          290;
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Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kinura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yanamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Suyawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Kikkawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
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Homo sapiens cDNA FLJ16830 fis, clone UTERU30
to Chromodomain helicase-DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                   1211 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGATACCTGTCCCC 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7 (Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Oto, Y., Hotuta, T., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Saco, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Tujii, A., Oshima, A., Sugiyama, A., Wagatsuma, M., Takahashi-Tujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
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Isogai, T. and Yamamoto, J.
Direct Submission
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   GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGGAG 1368
                                                              GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTG 689
                                                                                                                                                                                       GGGCCTTCCACCTGGCCTGCCCTGCCCTCCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                           GTGCTTACCACATGGTCTGCCTGGATTCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="UTERU3022536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="UTERU3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 58.8; DE; Pred. No. 0.2; 0; Mismatches
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AL611985
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES .
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101820 creccececire 101831
                                                                                                                                                                                                                       101700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                   533 GGACGAGTGTGCCGTGTGTCGGGAGGGGGGGGGGAGCTCATCTGCTGTGACGGCTGCCCCTCG 592
                                                                                                                                                                593 GGCCTTCCACCTGGCCTGTCCCCTTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG 652
                                                                                                                                                                                                                                                                                                                             86;
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AL611985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-421E12 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 23, 2002 this sequence version replaced gi:22797927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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                                                          GTGCTCCAGCTG 664
                                                                                                              CTCCTACCACTTGCACTGCCTCAACCCGCCGCTGCCGGAGATACCGAACGGTGAATGGCT 101819
                                                                                                                                                                                                                    GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTCCTGTGCTGTGATGCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP23-421E12"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .219205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                              3.8%;
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                                                                                                                                                                                                                                                                                                                                                 Score 58.4; DB 10;
Pred. No. 0.14;
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om clone RP23-421E12 on chromosome 4, complete
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RESULT 85
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                                                                                                                                                                                                      1209 GAG 1211
                                                                                                                                                                                                                                                      1149 GATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCTTCTGAGC 1208
                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                        60;
                                                                                                                                                                                                                                      μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-JUN-1996) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Tel:03-3351-3370, Fax:03-3351-2370)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagamine, K., Kudoh, J., Asakawa, S., Abe, I., Maeda, H., Tsujimoto, Minoshima, S., Ito, F. and Shimizu, N. Localization of 22 Exons to a 450-kb Region Involved in the Autoimmune Polyglandular Disease Type I (APECED) on Choromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kudoh, J., Nagamine, K., Abakawa, S., Abe, I., Kawasaki, K., Maeo Tsujinoto, S., Minoshima, S., Ito, F. and Shimizu, N. Localization of 16 exons to a 450-kb region involved in the autoimmune polyglandular disease type I (APECED) on human chromosome 21q22.3
                                                              Mus musculus chromodomain helicase DNA binding
                 BC060721.1 GI:38511411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagamine, K., Kudoh, J.,
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HC21EXc33.
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Homo sapiens gene for HC21EXc33,
                                                                                   BC060721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimizu, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21q22.3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                   (cDNA clone
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                                                                                                                                                                                                                                      GATGACACCGCCAGTCACGAGGCCGCTCTGCACAGGGATGAGCTGGAGTCCCTTCTGAGC
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                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                            /gene="HC21EXc33"
                                                                                                                                                                                                                                                                                                                                                                                                                          gene="HC21EXc33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome="21"
                                               IMAGE: 6406263), partial cds
                                                                                                                                                                                                                                                                                                                      3.8%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        _type="B-lymphoblastoid"
e_lib="chromosome 21-specific cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               line="GM130B"
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                                                                                                                                                                                                                                                                                                      Score 58.2; Di
Pred. No. 0.56
0; Mismatches
                                                                               4343 bp
                                                                                                                                                                                                                                                                                                                      No. 0.56;
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                                                                                   mRNA
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••
                                                                                                                                                                                                                                                                                                                                        Length 63;
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                                                               protein 3,
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                                                                                 ROD 25-MAY-2004
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Matches 102; Conserv
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIMI at: http://lmage.llnl.gov Series: IRAK Plate: 125 Row: f Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
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Direct Submission

Submitted (03-NOV-2003) National Institutes of Health, Mammalian Submitted (03-NOV-2003) National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodrique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AGGACGAGTGTGCCGTGTGTCGGGGACGGCGGGGGGGCTCATCTGCTGTGACGGCTGCCCTC 591
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                                                                                                                                                                                                                                                                            /tissue_type="Brain, enri
/clone_lib="NIH_BMAP_FOO"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE: 6406263"
                                                                                                                 3.8%;
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                                                                                  Score 58.2; DB Pred. No. 0.28; 0; Mismatches
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512

AGGATTACTGTGAGGTGTGCCAGCAGGGCGGGGAAATTATTCTGTGCGACACCTGCCCCC

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                                                                                                                                                                          AL Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 116984)
Birren, B., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Matthews, C., WcCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Mathews, C., WcCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Stedanan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 1, 2003 this sequence version replaced gi:27369450. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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HTG; HTGS_PH
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Bapiens chromosome 17 clone
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
                                                                                                                                                                                                    Mammalia; Eutheria; Pr
1 (bases 1 to 187718)
Birren,B., Nusbaum,C.
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                               Homo sapiens chromosome 17, clone
                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATTACTGTGAGGTGCCCAGCAGGGTGGGGAAATTATTCTGTGAGACACCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGCCCTCACTGTGTGAGTACCTAATGCCAGCATCTGATGGCCCTG 30927
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                                                                                                                                 (bases 1 to 187718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center code: WIBR
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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59.3%;
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41001: gap of 100 bp
78861: contig of 37860 bp
78961: gap of 100 bp
116984: contig of 38023 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-MAY-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 13, 2003 this sequence version replaced gi:29150453. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 1099_M_24
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                                                          complement(28149. .28277)
/rpt_family="Tigger4(Zombi)"
complement(28422. .28554)
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1675. .1676
/note="unresolved homopolymeric run:
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/rpt_family="MIR"
1582
 /rpt_family="MLTIG1"
complement(29134. .29251)
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complement(27834..27858)
/rpt_family="Tigger4(Zombi)"
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24851. .25513
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complement(23383...23
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complement(16991..17008)
note="<30 qual SNGL region"
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/rpt_family="MIR"
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11178. .11217
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10626. .10654
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clone_lib="RPCI-11 H
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ement(22667)
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Muzny, D.Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooke, S., Amin, A., Anguiano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brank, P., Buryell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
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AC111597.4 GT:24818936
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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complement(29321. .
/rpt_family="AluY"
29776 . .30152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34455. .34640
/rpt_family="MIR"
complement(34899. .35191)
/rpt_family="Alusx"
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complement(34143. .34263)
/rpt_family="AluJo"
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complement(33823. .33)
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7. .34147
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ement(2007)
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family="L2"
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ement(30860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .30508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .29644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 187718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                              HTG 09-NOV-2002
SEQUENCE, 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57831
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REFERENCE AUTHORS TITLE

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Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ TITLE
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AUTHORS
TITLE
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Checko, J., Chawas, D., Chen, G., Chen, Y., Chen, Z., Chu, J.

Cavila, M.L., Chocke, C., Docker, C., Chyle, M., Cree, N., Dedetich, D., Davila, M.L., Devis, C., Decamo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Dennen, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Depager, H., Dugan, Rocha, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Braper, H., Bougan, R., Escatto, M., Bigene, C., Escanc, C., Falls, T., Falls, T., Fan, G., Fernandez, S., Finley, M., Galsis, A., Garla, R., Garcia, A., Garner, T., Garza, M., Gebregeorgia, E., Geer, K., Gill, R., Gardy, M., Garrer, W., Guovara, W., Guarrer, D., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., S., Hadma, S., H., Hollins, B., Hoeells, S., Haldwis, S., Hadma, S., H., Hoggon, A., Bogese, M., Henderson, N., Hernandez, J., Garser, T., Garza, M., Gurarrer, D., Halland, W., Hamil, C., Hamilton, C., Hamilton, K., Warts, C., L., Lobow, H., Ewan, J., Idebird, D., Jackeon, A., Jackeon, A., Jackeon, A., Jackeon, A., Jackeon, A., Honderson, W., Hernandez, J., Hang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., L., Kovar, C., Karfit, C.L., Lebow, H., Ewan, J., Hang, H., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., L., Kovar, C., Karfit, C.L., Lebow, H., Ewan, J., Hang, H., Johnson, R., Halland, J., Karfit, C.L., Lebow, H., Ewan, J., Hang, H., Johnson, R., Johnson, R., L., Kovar, C., Karfit, C.L., Lebow, H., Ewan, J., Hang, H., Johnson, R., Halland, J., Karfit, J., L., Lebow, H., Ewan, J., Kang, H., Johnson, R., Halland, H., L., Lebow, H., Ewan, J., Hang, H., Johnson, R., Halland, H., L., Lebow, H., Ewan, J., Hang, J., Kang, J
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RESULT 89
AC115415
                                                                         SOURCE
                                                                                                                          VERSION
                                                                                                                                                ACCESSION
                                                                                                                                                                                             DEFINITION
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                                                                                                  KEYWORDS
                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72989 ATATGGAATTCTGTCGAGTCTGCAAGGATGGCGGGGAACTACTATGCTGTGACACCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
                                                                                                                                                261384 bp DN Rattus norvegicus clone CH230-164A18, ***, 2 unordered pieces. AC115415
                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                        AC115415
AC115415.3 GI:23266199
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                 Rattus norvegicus
                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                GGAGGTGCTCCAGCTG 664
                                                                                                                                                                                                                                                                                                                                                                                                                               TITCTTCCTACCATATCCACTGTCTGAACCCCCCCGCTGCCAGAGATCCCAAATGGCGAAT 73108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                         GGCTCTGTCCCCGCTG 73124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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27029
231728
231828
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Center clone name: CH230-150P11
Center clone name: CH230-150P11
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 198152 bases at least Q40
Consensus quality: 199686 bases at least Q30
Consensus quality: 200691 bases at least Q20
Estimated insert size: 204955; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-150P11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end_sequence:BH333066"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26928: contig of 26928 bp in length 27028: gap of unknown length 231727: contig of 204699 bp in length 231827: gap of unknown length 232984: contig of 1157 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                             SEQUENCING
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G IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Maiin, A., Anguiano, D., Alvolei, M., Baca, E., Badden, H., Baryant, M., Baryant, M., Baryant, M., Baryant, M., Baryant, M., Buhay, C., Barch, P., Barber, M., Barristead, M., Benahmed, F., Biswalo, K., Blair, J., Blandaranaike, D., Barber, M., Chen, Z., Chu, J., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cherch, D., Delgado, O., Denson, S., Deramo, C., Dingy, D., Dinh, H., Divya, K., Draper, H., Dugan, Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Eggan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagy, N., Forbes, L., Falls, T., Fan, G., Falls, T., Fan, G., Falls, Y., Gabrish, A., Garcia, M., Garc
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-MAR-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 261384)
Rat Genome Sequencing Consortium.

Direct Submission
                                                                                                                                                 On Sep 21, 2002 this sequence version replaced gi:21737235. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 261384) Worley, K.C. Direct Submission
                                                                                                                                                                                                                                                                                                  Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 261384)
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RESULT 90
AC123167/c
    ACCESSION
VERSION
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                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                      162918 GÉCTCTGTCCCCGCTG 162933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 ATGAGGACGAGTGTGCCGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCC 588
Rattus norvegicus clone CH230-70G17,
***, I unordered pieces.
AC123167
AC123167.4 GI:24635638
                                                                                                                                                                              AC123167
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCTTCCTACCATATCCACTGTCTGAACCCCCCGCTGCCAGAGATCCCCAAATGGCGAAT 162917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGGGCCTTCCACCTGGCCTGCCCTTCCCGCTCCGGGAGATCCCCAGTGGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGTGCTCCAGCTG 664
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Center clone name: CH230-164A18
Center clone name: CH230-164A18
Center clone name: CH230-164A18
Center clone name: CH230-164A18
Center clone name: Phrap; version 0.990329
Centersus quality: 215637 bases at least Q40
Centersus quality: 21565 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
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142337. .242648
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clone_end:T7"
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-164A18"
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                                                                                                                                                                              278068 bp
                                                                                                                                     DNA linear
7, *** SEQUENCING
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 6, 2002 this sequence version replaced gi:23664632.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                              Submitted (29-MAY-2002) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA 3 (Dases 1 to 278068) Rat Genome Sequencing Consortium. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
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Baylor College
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Center clone name: CH230-70G17
Center clone name: CH230-70G17
Center clone name: CH230-70G17
Center clone name: Phrap; version 0.990329
Consensus quality: 247200 bases at least Q40
Consensus quality: 251369 bases at least Q30
Consensus quality: 254516 bases at least Q20
Consensus quality: 254516 bases at least Q20
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/note="clone_boundary
clone_end:T7
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/note="clone_boundary
clone_end:T7
                                                              end_sequence:BH274648"
7361..64450
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                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                 clone="CH230-70G17"
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262126: contig of 1050 bp in length
262126: gap of unknown length length
263253: contig of 1027 bp in length
263253: gap of unknown length
263353: gap of unknown length
263311: contig of 1878 bp in length
266773: contig of 1442 bp in length
266773: contig of 1442 bp in length
266797: contig of 1124 bp in length
266997: gap of unknown length
268097: gap of unknown length
268097: gap of unknown length
268164: contig of 1124 bp in length
268164: contig of 1067 bp in length
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91481: gap of unknown length
236448: contig of 144967 bp in length
236548: gap of unknown length
250659: contig of 14111 bp in length
250759: gap of unknown length
260976: contig of 10217 bp in length
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236548:
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270430: contig of 1166
270530: gap of unknown
278068: contig of 7538
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare
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                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-APR 2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1sA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 5, 2004 this sequence version replaced gi:45433987.
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                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 189081)
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Pred. No. 0.19;
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526 AGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCT 58
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                                                                       110;
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CQ721455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subslones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where
                                                                                                                                                                                                                                                                         Patent: WO 02068579-A 7389 06-SEP-2002; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                     Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and oth
                                                                                                                                                                                                                                                                                                                                                                              Venter, C.J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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7389 from Patent WO02068579.
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-57K11"
                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                  Score 56.6; DB 6;
Pred. No. 0.62;
0; Mismatches 89;
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Submitted (28-MAR-1997) Osamu Ohara, Kazusa DNA Research Institute;
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfookazusa or.jp, Tel:+81-438-52-3913)
On Dec 23, 1999 this sequence version replaced gi:2224536.
Sequence updated (20-Dec-1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 6505)
Ohara,O., Nagase,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prediction of the coding sequences of unidentified human VII. The complete sequences of 100 new cDNA clones from team code for large proteins in vitro DNA Res. 4 (2), 141-150 (1997)
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Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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AB002296.2 GI:6634008
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/translation="Celiscpgcervyltrdytehfflhcyfteopkmarncseckek raahtlctychkmlcsscteekeksyvpggpfpfraokgspgvbgdftlycplht oevlictychklctychkltsctychklthctychkltheceplopklycplhteopklklfcbltebelgolgerpfraokgspgvbgdfydahkksslogtrefedenglefereplongerleggpfydahkkslborakcjerchefetedklcheeplongerleggpfyskoledrieleggptydengkleggpfyghgspradbespgglogsprydhgerpfraokgleggpfyghgspadgeberggradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspadgebergradbapaygglogsspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghgspfyghg
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Start codon is not identified, hf00341 cDNA clone for KIAA0298 has a 1857-bp insertion between 982-983, a 71-bp deletion at the region from 3002 to 3072, and a 290-bp deletion at the region from 3178 to 3467 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="KIAA0298"
<97. .2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hf003411"
                                                                                                                                                                                                                               /product="KIAA0298 protein"
/protein_id="BAA20758.2"
/db_xref="GI:6634009"
                                                                                                                                                                                                                                                                                                                                                                                           sequence of KIAA0298"
                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="KIAA0298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue type="brain"
clone_Tib="pBluescriptII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kikuno, R. and Nomura, N
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AUTHORS
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AF210315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beckstead,R., Ortiz,J.A., Sanchez,C., Prokopenko,S.N., Chambo
Losson,R. and Bellen,H.J.
Bonus, a Drosophila homolog of TIF1 proteins, interacts with
nuclear receptors and can inhibit betaFTZ-F1-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 5811)
                                                                                                                                                                                                                                                                                                                Submitted (01-DEC-1999) Molecular and Human Genetics/HHMI, Bay
College of Medicine, T634, Mail Stop BCM235, One Baylor Plaza,
Houston, TX 77030, USA
Location/Qualifiers
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AF210315
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Beckstead, R.B., Prok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription
Mol. Cell 7 (4), 753-765 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
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LSQTKSPGHLQQTIVGJINYIVRQPAPVQSQSQEETLQAFDEPBASQGSKEALPLDKU
TAAALPQASGEETPLSVPPUDSTIQHASPAVVRKHSTSLSIMGFSNTLEMELSSTLES
RPLEPQIQSVSNLTAGAPQAVPSLLSAPKMVSSLTSVQNQAMPSLTTSHLQTVPSLV
HSTFQSMPNLISDSPQAMASLASDHPQAGPSLMSGHTQAVPSLATCPLQSIPPVSDMQ
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                                                                 /gene="bon"
694. .4095
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DLSLTVLRPLMTTMSEFFDSCRHFTFERWKVRIPLASLTYWDKVP"
                                                                                                                                                                                                      /organism="Drosophila melanogaster"
|mol_type="m&NA"
|db_xref="taxon:7227"
|chromosome="3"
note="TIF1-like protein; BON"
codon_start=1
                                                                                                                                  gene="bon"
                                                 gene="bon"
                                                                                                                                                                               map="92E8-14"
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                                                                                                                                                               581
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                                                                                                                                                                                                                                                                                                                                                                                                                                Prokopenko, S.N. and Bellen, H.J.
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                                                                                                                                                                                                                                                                                                                                                             96;
 Drosophila
Drosophila
                                              CQ583074 6124 bp DN Sequence 10832 from Patent WO0171042. CQ583074 GI:41644029
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ALGLGPAVSILSNVTSTIPKTPSPSTHENTKOPTEPIDKVRDDSINDLIATIAKLDSN
GYQVLPEGRTKTTSPQVHSSTDLSNTQEVNNKNEQKDDPNEDWCAVCLDGGELMCCDK
CPKVPHQNCHIPAISSLPDESBSWQCLLCVNIKELTKYEGSEKSSSGELSALELETIQ
RICLELYCQYEGSLNFRSPESPANTSYYEIVSSPMSLDVIRTRLDPSSPNHYKDIAGF
VSDVRLIFSNTYLFYQEDTKTYSNAKYLENFFEEQLAKWLPQFEGTKPQGKRNTSNSP
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1225. .1338
/gene="bon"
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1411. .1506
/gene="bon"
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3571. .3909
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/db_xref="GI:6631000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="bon"
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                                                                                                                                                                                                  96;
                                                                                                                                                                                                                                                                                                                                                           Venter, J.C., Adams, M., Li, P.W. and Myers, E.W. Detection kits, such as nucleic acid arrays, for expression of 10,000 or more Drosophila genes and Patent: WO 0171042-A 10831 27-SEP-2001; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila sp.
Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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CQ583073
CQ583073.1 GI:41644028
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GAGAGCTGGCAGTGCCTACTGTGCGTCAACATCAAGGAGCTG
                                                                                     CTCGGGCCTTCCACCTGGCCTGCCTGCCTCCGGCTCCGGGAGATCCCCAGTGGGACC
                                                                                                                                AACGAGGACTGGTGCCCGTCTGTCTGGATGGAGGCGAGCTGATGTGCTGCGACAAGTGT 17865
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                                TEGAGETECTCCAGCTECCTECAGECAACAGTCCAGGAGGTE
                                                                CCCAAAGTTTTCCATCAGAACTGTCACATCCCTGCGATCAGCTCGTTGCCGGACGAGAGC
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                                                                                                                                                                                                                                                                          /organism="Drosophila sp."
/mol_type="unassigned DNA"
/db_xref="taxon:7242"
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/mol_type="unassigned
/db_xref="taxon:7242"
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1. .21747
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Pred. No. 0.49
0; Mismatches
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Pred. No. 0.6;
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ACCESSION
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Matches 96
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Sphydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 170339)

3S Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Bussm, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, J.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, B., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
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This sequence was identified as CDM:10212734 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 97538)
Adams, M. and Venter, J.C.
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AC017943
AC017943.1 GI:6553247
HTG; HTGS PHASE2.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                      melanogaster
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Pred. No. 0.38
0; Mismatches
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SEQUENCING IN PROGRESS
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  AUTHORS
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                                                                                                                                                                                                                                      AC007771 197071 bp DNA Drosophila melanogaster, chromosome 3R, BACR26M03, complete sequence.
                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-JUN-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 15, 2001 this sequence version replaced gi:6598748.
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                                                                                                                                                                         HTG
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Celniker, S.E.,
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/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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/db_xref="taxon:7227"
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|mol_type="genomic DNA"
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59.3%;
  Adams, M.D.,
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location For further information about this sequence visit our sequence

For further information about this sequence, please visit our sequence

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Drosophila melanogaster chromosome complete sequence.
AE003731 AE002708 AE014297
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RS Adams, M.D., Celniker, S.E., Holt, R.A., Wans, C.A., Gocayne, J.D., Amanatidee, P.G., Scherer, S.E., Li, P.W., Hookins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Aehburner, M., Henderson, S.N., Stuton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeifer, B.D., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeifer, B.D., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkon, C., Baldwin, D., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkon, C., Baldwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayaktaroglu, L., Beasley, E.M., Benson, K.Y., Benson, P.V., Berman, B.P., Bhandari, D., Botshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Broktein, P., Brottier, P., Bandari, D., Brottier, P., Bardari, D., Brottier, P., Bardari, D., Brottier, P., Bardari, D., Brottier, P., Davies, P., Cayley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dukov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferraz, C.
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Celniker, S.E., Wheeler, D.A., Kronmiller, B., Carlson, J.W.,
Halpern, A., Patel, S., Adams, M., Champe, M., Dugan, S.P., Frise, B.,
Hodgson, A., George, R.A., Hoskins, R.A., Laverty, T., Muzny, D.M.,
Nelson, C.R., Pacleb, J.M., Park, S., Pfeiffer, B.D., Richards, S.,
Sodergren, B.J., Svirskas, R., Tabor, P.E., Wan, K., Stapleton, M.,
Sutton, G.G., Venter, C., Weinstock, G., Scherer, S.E., Myers, E.W.,
         Annotation of the Drosophila melanogaster euchromatic genome: a systematic review Genome Biol. 3 (12), RESEARCH0083 (2002)
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Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster suchromatic genome sequence
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Location/Qualifiers
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The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective Genome Biol. 3 (12), RESEARCH0084 (2002)
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Submitted (06-SEP-2002) University of California
Sciences Addition, Berkeley, CA 94720, USA
7 (bases 1 to 230001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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ms,M.D., Celniker,S.E.,
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10974.771 Million cell updates/sec
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                                   AGCCACCCGTGGAGACCCCCGCTCCCCCCGGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAG
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standard; DNA; 1463

ВP

24-JUN-1999 (first entry)

cDNA encoding þ human autoimmune regulator-3 (AIR-3) protein

Autoimmune regulator-3; AIR-3; immune maturation; immune response; disease; autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular syndrome type I; APS I; 88.

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Location/Qualifiers 237. 1001 /*tag= a

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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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AAX26936 standard; DNA; ВÞ

AAX26936;

24-JUN-1999 (first entry)

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Best Local Similarity
Matches 1026; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes an autoimmune regulator-1 (AIR-1) protein. The AIR polypeptides and polynucleotides can be used in methods for the diagnosis and treatment of diseases related to immune maturation and regulation of immune response towards self and nonself. They can be used particularly in the diagnosis and treatment of autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED) (also known as autoimmune polyglandular syndrome type I (APS I))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2036 BP; 359 A; 718 C; 649 G; 310 T; 0 U; 0 Other;
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P-PSDB; AAY01712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Autoimmune regulator 1 (AIR1) DNA sequence
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                                                        ACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCCGCTGCCAGGTCTGGAC
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                                   ACTOTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGGCTGGAC
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AAX58605 standard; CDNA; 2245 ВP

(first entry)

Human autoimmune polyglandular disease type 1 (APGD1) cDNA

Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular disease type 1; APGD1; AIRE; human; transcription factor; autoimmune disease; diagnosis; gene therapy; ss.

variation /*tag= a /product= "human_APGD1" replace(358,T) /*tag= k replace(374,G) /*tag= 1 Location/Qualifiers replace (708, T)

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02-OCT-1997;
08-OCT-1997;
12-NOV-1997;
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P-PSDB; AAY06073
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                                                         97EP-00117154.
97EP-00117398.
97EP-00119810.
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/note= "alters !
protein"
                                                                                    98WO-EP006294
                                                                                                                      starts at this position"
2191. 2195
/*tag= t
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/note= "silent polymorphism"
replace(801,T)
/*tag= p
/*tag= p
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truncated 478 aa protein"
replace(1317,T)
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/note= "silent polymorphism"
replace(1365,C)
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/*tag= d
                                                                                                                                                                                                                                                                                                        replace (1094, A)
                                                                                                                                                                                                                                                                                                               truncated protein"
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truncated 371 aa protein"
replace(1090,CCTG)
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/note= "13-nucleotide deletion, results in frameshift
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/note= "silent polymorphism"
/eplace(889,T)
                                                                                                                                                                              replace (1698, T)
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/note= "1-nucleotide
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"1-nucleotide deletion"
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oo M, Lehracl
                   Lehrach
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New polypeptide which co-segregates ä mutated

Claim 1; Fig 2A; 77pp; English

polypeptides co-segregate with autoimmune polyendocrinopathy candidiasis cocodermal dystrophy (APECED). The invention provides vectors and host cells for preparation of APGDI polypeptides. APECED-associated mutations found in the APGDI gene include: an insertion of 4 nucleotides (CCTG), normally found at position 1086-1089, at nucleotide position 1085 or 1090 c; an insertion of an adenosine at position 1284; an insertion of a cytosine at position 1355; a deletion of nucleotides 1085-1097; a cytosine at position 1355; a deletion of nucleotides 1085-1097; a cytosine at position 1309 or 1313; a cytosine to thymidine exchange at position 358; an adenosine at position 368; a guanosine to thymidine exchange at position 358; an adenosine to guanosine to thymidine exchange at position 358; an adenosine to guanosine exchange at position 1052; and a cytosine to adenosine to adenosine to position 1094. A cytosine to adenosine exchange at position 1052; and a cytosine to adenosine exchange to position 1094. A cytosine to adenosine exchange to position 1094 and cytosine to adenosine exchange to position 1094. A cytosine to adenosine exchange to position 1094. A cytosine to adenosine exchange to position 1094 and cytosine to adenosine exchange to position 1094. A cytosine to adenosine exchange to position 1094 and cytosine to adenosine exchange to position 1094. A cytosine to adenosine exchange to position 1094 and cytosine to to thymidine exchange to thymidine excha This is the nucleotide sequence of human autoimmune polyglandular disease type 1 (APGD1 or AIRS) cDNA. It is a composite of 2 clones, which were obtained from a human adult thymus cDNA library by PCR (see AAYS669-10) and of a 3'UTR extension PCR product. The encoded protein (see AAY06073) is a transcription factor or transcription associate discort that may associate with vimentin fibres, perhaps as part of a docking mechanism regulating nuclear translocation. Aggregates of the mutated protein may prevent formation of vimentin intermediate filaments. Mutated APGD1 therapy or 1090

Sequence 2245 BP; 419 A; 765 C; 697 G; 364 T; 0 U; 0 Other;

2

Length

Matches 1026; 1351 1291 1231 1171 1111 1051 1411 876 816 936 756 696 Similarity CTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGC 575 CGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCC CCCAGTGGGACCTGCAGCTCCAGCTGCCTGCAGCAACAGTCCAGGAGGTGCAGCCC GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCCGGGACGGGCCTG GGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCC TCCTCGGCCCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCT TCCTCGGCCCTGCACCCCCTACTGTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCT ACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGGCTGGAC ACTCTTGTCTACAAGCACCTGCCGGCTTCCGCCTTCTGCAGCCCCGCCTGCCAGGTCTGGAC AGGTCGGCGGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACG AGGTCGGCGGAGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCCGGCATGGACACG CGGGCAGAGGCCCCGGGCCCCAGGAGCCCACCCGTGGAGACCCCCGCTCCCCCGGGGGCTT CGGGCAGAGGAGCCCCGGCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCCCGGGGCTT CCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCC TGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATC TGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATC CTCCACCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGC Conservative 66.3%; <u>,,</u> Score 1023.6; DB 2 Pred. No. 1.1e-208; Mismatches Indels 0, Gaps 1470 1055 .995 1410 935 1350 1290 1230 1170 1050 1530 875 815 695 1110 635 755 0

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08-OCT-1997;
12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse autoimmune polyglandular disease type 1 (APGD1) cDNA
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                                                     WPI; 1999-287735/24.
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Best Local Similarity
Matches 580; Conserv
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Claim:6; Fig 14A-C; 77pp; English.

This is the nucleotide sequence of murine AIRE cDNA. Murine AIRE is the homologue of the human AIRE (or autoimmune polyglandular disease type 1, APGDI) gene (see AAX58605). The overal nucleotide sequence identity between the mouse AIRE coding sequence and that of the human is 76.67%. The mAIRE gene was localised to chromosome 10. Human mutated APGDI cosegregates with autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECB). The murine homologue may be used to develop an animal model for APECBD, to examine the events that lead to the development of APECED and possibly to develop agents for preventing and/or treating this autoimmune disease

Sequence 1656 BP; 344 A; 532 C; 479 G; 301 T; 0 U; 0 Other;

Conservative

25.0%;

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Indels Length 1656;

Gaps

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TAGTCACGACCCTGTTCTACATAGGGACGACCTGGAGTCCCTCCAATGAGCACTCATT
                       TGTACCCACCTCTGGGCCCCGTCCAGCACCTGGGCTTGCCAAGGTAGGGACGACTCTGC
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Pred. No. 1.3e-72;
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CGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCCCGTCCGGCGGCCCCCTTCCCCTC

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                                                                                                                             Query Match
Best Local S
Matches 146
                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cycosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvilsant; ophthalmological; neuroprotective; antiarthritic; antidiabetic; antisporiatic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                             macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL32092 standard;
                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2001; 2001WO-EP007537
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                                                                     9386
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                                          61
                                                                                                                              146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system disease; cytosine methylation;
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 65; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCACGCCCGCTGGCCGAGACACCACC
                                                                                         AGAGAAAGTGAGGTCTTCTCAGGCTCTTAAGAGCATGGCGTTTTGGTCCAGGCTGTACCCG
             TTGTTTTTAGTTGGGTTCGTGGGTTGGGTCGGCGTTTTTGTTATAGTTAGGAGGTTAAGG
                                       crecrereaecreeecreeereeecreeecreecrecraraeccaeeaeercaaee
                                                                      AGAGAAAGTGAGGTTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                      9876
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                                                                                                                                                                                                                                                                                                                                                                                          and treatment
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                                                                                                                           7.7%;
ilarity 76.0%;
Conservative
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                                                                                                                                                                                     BP; 1912 A; 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                       fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
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                                                                                                                             <u>,</u>
                                                                                                                             Score 118.4; DB (
Pred. No. 1.6e-15;
0; Mismatches 40
                                                                                                                                                                                     C; 2928 G; 4727 T;
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                                                                     TAAGAGTATGGCGTTTGGTTTAGGTTGTATTCG
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                                                                                                                                                                                   0 U; 0 Other;
                                                                                                                             Indels
                                                                                                                                                      Length 9876;
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RESULT 7
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                                                                                                  Query Match
Best Local Similarity
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antitheumatic; antiatriric; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                          macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                           Nucleic acid comprising diagnosis and treatment methylation.
                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL32093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL32093
                                                                                                                                        Sequence
                                                                                                                                                                                                                               genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17
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                                                                                                                                                                                                                 including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic;
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                                    491
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         61
                                                                                                                                                                                                                                                                                                                                                                                                                EPIGENOMICS
CTGCTCTCAGCTGGGCCCGTGGGTGGGCCGGGCGCCCCTGCTATAGGCCAGGAGGTCAAGG
                                    AAAAAAAATAAAATCTTCTCAAACTCTTAAAAACATAACGTTTAATCCAAACTATACCCG
                                                                                                                                          9876
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                                                                                                                                                                                                                                                                                    SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGTGTGGGGG
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                                                           AGAGAAAGTGAGGTCTTCTCAGGCTCTTAAGAGCATGGCGTTTGGTCCAGGCTGTACCCG
                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          2000DE-01032529.
2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                        B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system disease; cytosine methylation;
                                                                                                                                                                  present sequence is a gene
                                                                                                                                        1882 A; 309 C; 3154 G;
                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                  6.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                  32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                        fragment of of diseases
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                                                                                                                                                                                                                                                                                                                                                                                        Berlin
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                                                                                                  Score 101.8; DB 6
Pred. No. 5.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      ζ.
                                                                                                                                                                                                                                                                                                                        chemically modified gene, associated with abnormal
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                                                                                                                                        4531 T; 0 U; 0 Other;
                                                                                                                                                                  of the invention
                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nootropic;
                                                                                                                                                                                                                                                                                     German.
                                                                                       Indels
                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiasthmatic;
                                                                                                                                                                                                                                              The sequences
                                                                                      ۰,
                                                                                                                                                                                                                                                                                                                           cytosine
                                                                                                                                                                                                                                                                                                                                       useful for
                                                                                     Gaps
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CTACTCTCAACTAAACCCGTAAATAAACCGAACGCCCCTACTATAACCAAAAAATCAAAA

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The invention relates to human chromodomain, helicase, DNA-binding 5 CC (CHD5; ADH12180) and cDNA encoding it (ADH12179). CHD5 is a novel member of the CHD gene family, members of which have a profound effect on cof the CHD gene family, members of which have a profound effect on the coff that is tructure and gene expression and which are thus likely to play cofficient in the comprises two N-terminal zinc finger domains of the PHD companies of the CHD5 comprises two N-terminal zinc finger domains of the PHD companies of the CHD5 companies of the PHD contains a predicted DEAH-box-type helicase domain and a putative SNF2 commain, and several nuclear localisation signals. The gene encoding CHD5 is located on chromosome 1p56.3, a region frequently deleted in a variety coff cancers including neuroblastoma, and the protein is preferentially capterssed in brain. CHD5 is therefore thought to be a modulator of normal neural development and neoplasias of neural tissue origin. The invention calso relates to vectors and host cells comprising the CHD5 cDNA sequence, an antibody against CHD5; a method of screening for modulators of CHD5 cativity; a method of diagnosing cancer in a patient, where a reduced companies of CHD5 or CHD5 or CHD5 nucleic acids indicates the presence of CHD5 countered and companies of chost calls cancer a reduced continue of the companies of the presence of CHD5 or CHD5 nucleic acids indicates the presence of CHD5 countered countered and countered coun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromodomain helicase DNA-binding 5; CHD5; chromosome 1p36.3; chromatin structure; chromatin unwinding; DNA repair; DNA recombination; transcriptional regulation; gene expression; cell cycle control; development regulation; oncogenesis; brain; neural development; neural tissue neoplasia; diagnosis; cancer; neural cancer; neuroblastoma; breast cancer; colon cancer; liver tumour; germ cell tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel chromodomain helicase DNA-binding (CHD) proteins, useful as diagnostic and prognostic indicator of tumor, comprises amino terminus having two PHD class zinc finger domains and two chromodomains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brodeur GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening; cytostatic; gene therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH12180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1; 124pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0388848P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product= "CHD5"
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Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; treating cancer by administration of CHD5 protein, CHD5-encoding nucleic acids or CHD5 mimetics; and CHD5-specific PCR primers (ADH12186-ADH12247). The methods of the invention are useful in the diagnosis or treatment of cancers such as neural cancers (e.g., neuroblastoma), breast cancer, colon cancer, liver tumours and germ cell tumours. The CHD5 protein, CHD5 nucleic acids and anti-CHD5 antibodies are useful as research tools to identify other proteins that are intimately involved in chromatin unwinding, DNA repair and recombination, and transcriptional
                                                                                                                                                           New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000US-0221607P
02-MAY-2001; 2001US-0287724P
                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; rat; splice transcript; detection; RNA transcript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9646 BP;
                                                                                                                  Example 1; SEQ ID NO 11363; 47pp; English
                                                                                                                                                                                                                           WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                               20-JUL-2001; 2001WO-IB001903
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200210449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splice variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN38615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN38615 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation. The present sequence represents cDNA encoding human CHD5.
                                                                                                                                                                                                                                                                                    (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAGATCATCCTGTGCGACACCTGCCCGA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGACGAGTGTGCCGTGTGTCGGGACGGCGGCGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCCCCCACTGTGAGAAGGAGGGGATCCAGTGGGAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.2%;
ilarity 62.7%;
Conservative
                                                                                                                                                                                                                                                        Wasserman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcript detection oligonucleotide SEQ ID NO:11363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcriptome; oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2076 A; 2789 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                                                                                                                                                                                                                                        Mintz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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Pred. No. 0.0004;
0; Mismatches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3013 G; 1768 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 9646;
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                                                                                                                                                                                                                                                      Faigler
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridisting selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The

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RESULT 10
ABK70271
ID ABK70271
AC ABK70
XX ABK70
XX IS-JU
DE Human
XX Human
XX Homo
XX 28-MA
XX WPI;
XX MPI;
XX MPI;
XX MPI;
XX The i
CC The i
CC Selec
CC Or th
CC Selec
CC The j
CC Polly
CC Dolly
CC Polly
CC P
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Best Local S
Matches 60
                           The invention relates to an isolated polynucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the polynucleotide operably linked to an expression control sequence, a host cell transformed or transfected with an expression vector of; an isolated antibody, or its antigen-binding fragment that specifically binds to the polypeptide; a method for detecting the presence of a cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tumor lung proteins and nucleic acids encoding the proteins, us as vaccines and for treating, preventing, diagnosing or monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-2000; 2000US-0234837P
10-OCT-2000; 2000US-0239440P
29-JUN-2001; 2001US-0301928P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lung cancer associated full length cDNA DMSM-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK70271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

    and pathology-specific genes such as those genes only expressed
specific tissue under a specific pathological condition; to detect

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minitranscriptome under a particular libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-372001/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-)
fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                Page 146-148; 189pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 13 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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   comprising at least the polypeptide; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No.
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC oligonucleotide that hybridises to the polynucleotide under moderately crimgent conditions; a method for stimulating and/or expanding T cells specific for a tumour protein; an isolated T cell population comprising T cells prepared from the method of above; a composition comprising a first component consisting of carriers and immunostimulants, and a second component selected from the polynucleotides, proteins, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the composition; and a second component in a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotide of, or an antibody and a detection reagent consisting of a reporter group. The polypeptides and composition reagent consisting of a reporter group. The polypeptides and composition content or prevention of compositions and in the presenting cells can be used to stimulate or expand T cells specific for a tumorous protein. The coplynucleotides may be used as probes or primers for nucleic acid contents of the present sequence is one of the 183 lung cancer associated contents of presents sequence is one of the 183 lung cancer associated contents of the present sequence is one of the 183 lung cancer associated contents of the present sequence is one of the 183 lung cancer associated contents of the present sequence is one of the 183 lung cancer associated contents of the present sequence is one of the 183 lung cancer associated contents of the present sequence is one of the last lung cancer associated contents of the present associated contents of the last lung cancer associated contents of the present sequence is one of the last lung cancer associated contents of the l
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Best Local S
Matches 96
                                                                                                                                                                                                                                         3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermatomyositis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mi-2; autoantigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT32301;
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  15-MAR-1995;
                                           15-MAR-1995;
                                                                                                                                 DE19509279-C1
                                                                                                                                                                                         polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dermatomyositis specific autoantigen, Mi-2, coding sequence
                                                                                      15-MAY-1996.
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95DE-01009279
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6234. .
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                                                                                                                                                                                                                                                             given starts at nucleotide
                                                                                                                                                                                                                                                                               /product= "Mi-2"
/note= "the first ATG is at nucleotide 90,
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen disease; chromosome 12; 12p13; helicase;
iagnosis; ss.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
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                                                                                                                                                                                                                                                                                      the sequence
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RESULT 12
ABL64410
ID ABL644
XX ABL64
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Best Local
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05-JUN-2000;
05-JUN-2000;
18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen, designated Mi-2. The sequence numbering given in the specification starts at nucleotide 91, i.e. the 5' UTR is omitted, as well as the 'A' of the first ATG start codon. The protein is hydrophilic, acidic and protruding regions of the protein are characteristic of helicases. The gene corresponding to this CDNA was localised to chromosome 12 (12p13). The DNA can be used for the recombinant production of Mi-2 which is used for, e.g. the differential diagnosis of collagen diseases, esp. dermatomyositis, e.g. by immunoassay or Western blotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; co
stomach; lung; pi
cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stomach cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6327 BP; 1761 A; 1473 C; 1740 G; 1353 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding dermatomyositis specific auto:antigen - useful differential diagnosis and treatment of dermatomyositis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL64410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL64410 standard; DNA; 6417 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGACGAGTGTGCCGTGTCGGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCTTCCACCTGGCCTGCCCTGCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1263
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                         7 2000US-0209473P.
2000US-0209531P.
2000US-0233131P.
2000US-0233617P.
2000US-0234034P.
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2000US-0234034P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon; breast; ovary; oesophagus; kidney; thyroid;
prostate; pancreas; carcinoma; antitumour; cancerous;
ne therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related gene
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Pred. No.
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                                                                                                                                                                                                               (AVAL-) AVALON PHARM
                                                                                                                                                                                          PE,
                                                                                                                                                                                          Augustus
Weaver Z
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2000US-0237608P.
2000US-0244867P.
2000US-0245084P.
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2000US-0235720P.
2000US-0235843P.
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2000US-0234923P.
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                                                                                                                                                                                                  Carter
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                                                                                                                                                                                                  Ebner
                                                                                                                                                                                                  Endress
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change expression of a gene of a signature gene Bet.

Claim 1; SEQ ID NO 2747; 44pp; English.

neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's The present invention describes a method (M1) for screening for an

Sequence 6417 BP; 1774 A; 1494 C; 1784 G; 1365 T; 0 U; 0 Other;

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Query Match
Best Local S
Matches 96
 96;
          Similarity
 Conservative
        3.9%;
Score 60; DB 6
Pred. No. 0.004
0; Mismatches
          0.0044;
                  9
  60;
                  Length
  Indels
                  6417;
 0
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RESULT 13
ABX04169
AD ABX04
AX
AX
ABX04
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AX
ABX04
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AX
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             The invention relates to new isolated nucleic acid molecule comprising nucleic acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a chondroblastic pharacture of the third form mesenchymal cell to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chondroblastic phenotype; mesenchymal cell; cartilage formation; bone formation; arthritis; osteoarthritis; rheumatoid arthritis; gout arthritis; adjuvant arthritis; arthritis deformans; antigout; infectious arthritis; osteochondrossis; RDA; antiarthritic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnosing and treating cartilaginous tissue degeneration conditio e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX04169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 111-113; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizuno S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skeletal growth; cartilage degeneration disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA; 6417
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genes
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         technique of representational difference analysis, RDA), its expressiproducts or fragments, fixed to a solid substrate. The nucleic acids, polypeptides and agents are useful for treating cartilaginous tissue degeneration conditions such as osteoarthritis, rheumatoid arthritis, gout arthritis, adjuvant arthritis, arthritis deformans, infectious arthritis, arthritis deformans, infectious arthritis, or osterochondrosis. The present sequence is a CDNA from a known gene differentially expressed in developing mesenchymal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6417 BP; 1774 A; 1494 C; 1784
                                                                                                                                                                                        Beazer-Barclay Y,
                                                                                                                                                                                                                                                 03-OCT-2000; 2000US-0237189P
                                                                                                                                                                                                                                                                          03-OCT-2001; 2001WO-US030821
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #1267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK84696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK84696 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentially expressed in developing mesenchymal cells using
                                                                                                                                                                                                                                                                                                                                   WO200228999-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                   GENE LOGIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                        Weissman
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                        Yamaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 1365 T; 0 U; 0 Other;
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                                                                                                                                                                                        Vockley
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the

à

expression

expression

unactivated

Claim

SEQ

ID NO

1267; 114pp; English

Detecting granulocyte activation by detecting differential expression genes associated with granulocyte activation, which serves as diagnost markers that is useful for monitoring disease states and drug toxicity

xpression of singular diagnostic glassicity.

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RESULT 15
AAD54631
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6417 BP; 1774 A; 1494 C; 1784 G; 1365 T; 0 U; 0 Other
                                                                                                                                                                                                                                                              Human; p53 pathway; therapeutic; angiogenic disorder; apoptotic disorder; chromodomain helicase DNA binding protein; CHD; cancer; gene therapy; cell proliferative disorder; chromatin organisation modifier domain;
                                                                                                                                                                                                                                                                                                                                                                                      Human chromodomain helicase DNA binding protein (CHD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD54631 standard; DNA; 6417
                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2003
                                                        12-DEC-2002
                                                                                                                    WO200298899-A2
                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 AGGACGAGTGTGCCGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
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Pred. No. 0.0044;
0; Mismatches 6
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03-JUN-2002; 2002WO-US017466.

12-DEC-2002

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RESULT 16
AAD54632
ID AAD54
XX AAD54
XX AAD54
XX AAD54
XX Human
XX Human
XX Human
XX Cell
XX Chrom
KW Cclo
XX Colo
XX Oyloo
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Best Local
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10-OCT-2001;
22-OCT-2001;
15-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway modulating agents. The method involves contacting an assay system comprising purified chromatin organisation modifier (chromo) domain helicase DNA binding proteins (CHD), nucleic acids, their functionally active fragments or derivatives, with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity. The methods are useful for identifying modulators of the p53 pathway as therapeutic targets for disorders associated with defective p53 function, such as angiogenic disorders, apoptotic disorders or cell proliferative disorders, e.g. cancer. The modulators are useful as research reagents, diagnostics and therapeutics. The invention is also useful in gene therapy. The present sequence is human CHD DNA
                                                                                                      Human; p53 pathway; therapeutic; angiogenic disc
chromodomain helicase DNA binding protein; CHD;
cell proliferative disorder; chromatin organisat
cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a candidate p53 pathway-modulating targets for disorders related to defective p53 contacting an assay system having purified CHD acid, with a test agent.
                                                                                                                                                                                                                                                                                                      AAD54632 standard;
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Lioubin MN;
                                     WO200298899-A2
                                                                                                                                                                                             Human chromodomain helicase
                                                                                                                                                                                                                                 26-JUN-2003
                                                                                                                                                                                                                                                                    AAD54632;
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                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for identifying candidate p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                             1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1198 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                               652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2001US-0296076P.
; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
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                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.9%;
                                                                                                                                                                                                                                                                                                       6417
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                                                                                                                                                                                           DNA binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                        eın; CHD; cancer; gene
organisation modifier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 6417;
                                                                                                                                                          disorder; apoptotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                                                                                                                                                                             1353
                                                                                                                                                                                                                                                                                                                                                                                                                               687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agent as therapeutic function e.g. cancer by polypeptide or nucleic
                                                                                                                                                                                               (OHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                           encoding DNA #7.
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                                                                                                                        therapy;
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RESULT 17
ADP10531
ID ADP10
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ADP10
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AC ADP10
DT 12-AU
DX
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KW trans
KW infla
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Homo
OS Homo
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PD 21-M2
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Matches 96
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10-OCT-2001;
22-OCT-2001;
15-FEB-2002;
15-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathway modulating agents. The method involves contacting an assay system comprising purified chromatin organisation modifier (chromo) domain helicase DNA binding proteins (CHD), nucleic acids, their functionally active fragments or derivatives, with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity. The methods are useful for identifying modulators of the p53 pathway as therapeutic targets for disorders associated with defective p53 function, such as angiogenic disorders, apoptotic disorders or cell proliferative disorders, e.g. cancer. The modulators are useful as research reagents, diagnostics and therapeutics. The invention is also
                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                           WO2004042346-A2
                                                                             transplant rejection; immune inflammatory bowel disease;
                                                                                                                   Reference
                                                                                                                                                                                                 ADP10531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate p53 pathway-modulating targets for disorders related to defective p53 contacting an assay system having purified CHD
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                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                         GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
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                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy. The present sequence is human CHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a method for identifying candidate p53
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                                                                                                                                               (first
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                                                                                                                   sequences
                                                                                                                                                                                                 DNA;
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                                                                                                                                             entry)
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                                                                                         immune system;
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                                                                              multiple
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Pred. No. 0.00
0; Mismatches
                                                                                                                   marker probe
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                                                                              rheumatoid arthritis;
sclerosis; HIV; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6417;
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RESULT 18
AA158444
ID AA158
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XX AA58
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XX Human
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Matches 96
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                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haæmostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection, e.g. cardiac or kidney transplant rejection, in an i-
comprises detecting the expression level of one or more genes,
methods, system and kits are useful in diagnosing or monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing or monitoring transplant rejection, epancreas, pancreatic islet, lung, bone marrow or rejection, in an individual, comprises detecting
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                                                                                                                                                              Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                              AAI58444 standard;
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                                                leukaemia; ss
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2002US-00325899.
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Homo sapiens

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RESULT 19
ADQ98655
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AC ADQ9
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AC ADQ9
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AC ADQ9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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25-APR-2000;
20-JUN-2000;
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Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6475 BP; 1760 A; 1528 C; 1822 G; 1365 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful as central nervous system injuries.
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                       23-SEP-2004
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03-AUG-2000;
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19-OCT-2000;
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Wang Z,
Goodrich
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2000US-00620312.
2000US-00653450.
2000US-00662191.
2000US-00693036.
2000US-00727344.
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ilarity 61.5%;
Conservative
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2000US-00552317.
                     (first entry)
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Wehrman T,
h R, Drmanac
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, Xu C,
ac RT;
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Pred. No. 0.
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Xue
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F,
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, Zhao QA;
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RESULT 20 ADB48415 ID ADB48

ADB48415 standard;

CDNA;

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04-DEC-2003

(first entry)

Novel human cDNA SEQ ID NO

325.

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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated polynucleotide (I) comprising a fully defined (S1) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041, 1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as given in the specification, its translated or protein coding portion, its extracellular portion or its active domain. The GPCR-like polypeptides and polynucleotides are useful for the treatment of diseases of ophthalmic, neurological, immunological and nephritic systems. They may also be used to treat hormonal dysfunction, cancer, atherosclerosis and dishbers.
                                                                                                                                                                                                                                                                                   Sequence 6475 BP; 1760 A; 1528 C; 1822
                                                                                                                                                                                                                                                                                                                                    diabetes. The antibodies are useful for detecting or quantitating the polypeptide in tissue. The polypeptides can also be used as molecular weight markers and as a food supplement. This sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New G-protein-coupled receptor-like polypeptides and polynucleotides, useful for treating diseases of ophthalmic, neurological, immunologic and nephritic systems and hormonal dysfunction, cancer, atheroscleros and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic; antidiabetic; GPCR-like protein; ophthalmic disorder; neurological disorder; mmunological disorder; nephritic disorder; hormonal dysfunction; cancer; atherosclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6569662-B1
                                                                                                                                                                                                                                                                                                                     polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 325; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442255/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human GPCR-like protein seqid 325
                                                                                                                                        1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC.
              GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
                                                                                                                                                             AGGACGAGTGTGCCGTGTGTCGGGACCGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                                                                                                   egecctrocacciegocitecorecoccitececiocegaaaarccccagiegaacciega 651
                                                                                                                                      AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                   GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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                                                                                                                                                                                                            3.9%;
ilarity 61.5%;
Conservative
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                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                   G; 1365 T; 0 U; 0 Other;
                                                                                                                                                                                                                               DB 5;
0.0044;
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                               687
                                                                                                                                                                                                                                               Length 6475
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atherosclerosis
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RESULT 21
AAI60230
ID AAI60
XX
AC AAI60
XX
DT 22-OC
DT 22-OC
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Human
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Humar
XW Humar
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Best Local Similarity
Matches 96; Conserv
        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide, userur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
19-JUL-2000; 2000US-00620312.
                                                                                                  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TANG/)
(LIUC/)
(ASUN/)
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                                                                                                                                                AAI60230 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html?DocID=20030104529.
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                                                                          polynucleotide
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TANG Y T.
LIU C.
ASUNDI V.
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                                                                                                                                                                                                           GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1482
                                                                                                                                                                                                                                     GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                                                                                                                                                                                                             GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                          6475 BP; 1760 A; 1528 C; 1822 G; 1365 T; 0
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                (first
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                                                                                                                                                cDNA;
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61.5%;
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grug
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Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
                                                                          4219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating
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                                                                                                                                                                                                                                                                                                                                                                        0.0044
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                                                                                                                                                                                                                                                                                                                                                           60;
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                                                                                                                                                                                                                                                                                                                                                                                  Length 6475;
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                                                                                                                                                                                                                                                                                                                                                                                                           Other
                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 22 ADQ22446 ID ADQ224 XX

ADQ22446

standard;

DNA;

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                                                                                                                                                  Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                    in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999;
21-JAN-2000;
25-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                             part
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369 encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L9-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                        central nervous
1424
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                                                                                                  1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                     AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                     6553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Asundi V, Wang Z, Wehrman T, Goodrich R, Drmana
                                                 GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                         GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                  AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG
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                                                                                                                                                3.9%;
nilarity 61.5%;
Conservative
                                                                                                                                                                                                                             printed specification
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2000US-00552317
2000US-00598042
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2000US-00727344
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2000US-00653450
                                                                                                                                                                                                     BP;
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system injuries.
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Xu C,
c RT;
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Pred.
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Xue
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                                                                                                                                                   60;
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                        687
                                                                                                                                                                           Length 6553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ϋ́, XΒ΄
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Zhang
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RESULT 23
AAQ22728
ID AAQ22
XX
AC AAQ22
XX
DT 25-MA
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25-MAR-2003
27-JUL-1992
                                 AAQ22728;
                                                      AAQ22728 standard; cDNA; 1053 BP
                                                                                                                                                                                                                                                                                            Sequence 6848 BP; 1848 A; 1585 C; 1873 G; 1431 T; 0 U; 111 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90ft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 5266; 210pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2002; 2002US-0429739P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human soft tissue sarcoma-upregulated DNA - SEQ ID 5266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-)
                                                                                                                                                                                                                                                             Local Similarity
                                                                                                               1380
                                                                                                                                                           1320
                                                                                                                                                                                                       1260
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                                                                                                                                                                                                                     532 AGGACGAGTGTGCCGTGTGTCCGGGACGCCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                                                                                                                                                                                                                                  96;
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                                                                                                                                                        GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                               GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCAGAGATCCCCAGTGGGACCTGGA 651
                                                                                                                                                                                                     AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ginsburg WM,
                                                                                                                                    GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                                                              GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sarcoma; cytostatic; gene therapy; vaccine; screening;
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(revised)
(first entry)
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Pred. No. 0.0044;
0; Mismatches 6
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ADF69743; 12-FEB-2004

(first entry)

ADF69743 standard;

CDNA; 1053 BP

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Matches 103;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      controls or from dermatomyositis patients contg. auto-antibodies other than anti-Mi-2. Clone L1 was used to screen sera from 40 patients. The CDNA was expressed. The insert was 1.1 kb and includes a single long open reading frame spanning the entire insert, in phase with beta galactosidase. Since there are no start or stop codons, the insert does not contain the entire gene. The clone may be used as a DNA probe to isolate DNA encoding additional portions of the human antigens. This DNA and the protein encoded by it may be used in immunodiagnostic assays to identify patients expressing anti-Mi-2 autoantibodies, and to diagnose dermatomyositis. See also AAQ22729,30. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human thrombocyte lambda gt 11 expression library was expressed in E. coli Y1090 and was screened with serum from a deratomyositis patient. This serum had previously been found to only contain anti- Mi-2 autoantibodies. A CDNA clone L1 was selected that expressed a protein which reacted with the anti-Mi-2 serum but not with the sera from normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1053 BP; 265 A; 256 C; 341 G; 191 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding myositis-specific antigen M1-2 - useful in diagnosing dermatomyositis and polymyositis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-114375/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1991;
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58.98;
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Pred. No. 0.
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RESULT 25
ABV23250
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Best Local S
Matches 103
Human; prostate cancer;
pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of human antigens Mi-2 and PM-Sc1, and the polynucleotide sequences encoding them. The human Mi-2 or PM-Sc1 proteins or a portion (at least one epitope) of them may be used in assays for diagnosing dermatomyositis, polymyositis or myositis-sclerosis overlap disorders. The present sequence encodes human Mi-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Mi-2 antigen; dermatomyositis; polymyositis; myositis-sclerosis overlap disorder; gene; ss.
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                                                                           Human prostate
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OKLAHOMA MEDICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                              (first
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                                                                           expression marker cDNA 23241.
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                     cancer; cytostatic; carcinogen;
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/note= "This sequence la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                  CDNA; 6331
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gene;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lacks both start and stop codons"
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                        pharmacodyanamic
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RESULT 26
ACD13374
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Best Local Similarity
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Human; ss; gene; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6331 BP; 1719 A; 1551 C; 1817 G; 1233 T; 0 U; 11 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                           Human DNA encoding
                                                                                                                                                                   13-AUG-2003
                                                                                                                                                                                                                         ACD13374;
                                                                                                                                                                                                                                                                               ACD13374
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18-JUL-2000;
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                   1466
                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 4195-4196; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGCCCTCACTGTGAGAAGGAGGGGGGTCCAGTGGGAGGCCCAAGGAGGAAGAAGA 1520
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; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%;
                                                                                                              p53 modifier, SEQ ID 44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.8;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6331;
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CC modulating agent, by contacting an assay system comprising a purified HM CC polypeptide (human orthologue of genes that modify the p53 pathway in CC Drosophila) or nucleic acid with a test agent under conditions, where but CC activity, and detecting a test agent, the system provides a reference CC activity, and detecting a test agent, biased activity of the assay system. CC Also included are modulating (M2) a p53 pathway of a cell (comprising CC contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising (M3) a p53 pathway of a gent that cC specifically binds an HM polypeptide comparising (M3) a p53 pathway of a disease in a patient (comprising contacting the cell with an agent that CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) CC a disease in a patient (comparising the sample with a probe for HM CC expression; (c) comparing the results with a probe for HM CC expression; (c) comparing the results with a probe for HM comparison indicates a likelihood disease). (M1) is useful CC in a patient, where the cancer has greater than 25 * expression level. CC in a patient, where the cancer has greater than 25 * expression level. CC defects in the p53 pathway. Buthway apolyotic or cell codefects in the p53 pathway. Buthway of a cell, thus restoring CC the p53 function of the cell, so that the cell cycle. (M2) and (M3) are useful in a variety of diagnostic and CC therapeutic progression through the cell cycle. (M2) and (M3) are useful or treating defects in the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, concertion activity and disorders. The present sequence is an HM cCC ancell proliferation disorders. The present sequence is an HM cCC ancell proliferation disorders. The present sequence is an HM cCC ancell proliferation disorders.
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2001; 2001US-0296076F
10-OCT-2001; 2001US-0328605F
15-FEB-2002; 2002US-0357253F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying (M1) a candidate p53 pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 269-271; 678pp; English
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                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid encoding a p53 pathway modifying protein
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GGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
                                                             GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
                                                                                                                          AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                                                                                             AGGACGAGTGTGCCGTGTCTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6331 BP; 1720 A; 1552 C; 1819 G;
                                                                                                                                                                                                                                                                                                                            larity 58.9%;
Conservative
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Pred. No. 0.0048;
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); Mismatches
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Sequence 6331 BP;

1720

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                                                              The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I; ADI26740-ADI26744 and ADI26766-ADI26769) from compositions of the expression of which is induced by an angiogenic agent, or its complement or fragment; polypeptide (II; ADI2679-ADI26793) able to inhibit and ADI2679-ADI26793 and Expression of (I); or an antibody (Ab) that binds (II). The compositions are used for treating a wide range of angiogenic diseases: tumour care used for treating a wide range of angiogenic diseases: tumour care used for treating a wide range of angiogenic diseases: tumour care used for treating a wide range of angiogenic diseases: crohn disease; atheroscilerosis; ovarian hyperstimulation; psoriasis; endometriosis associated with neovascularization; restenosis (arterial or after balloon angioplasty); overgrowth of cells in wound healing; peripheral vascular thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; convenie heart disease; (congestive) cardiac insufficiency; age-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                  muscular degeneration and osteoporosis. This sequence chromodomain helicase DNA binding protein 3 (CHD3).
                                                                                                                                                                                                                                                                                                                                                                                                                      Antiangiogenic composition, useful for treating e.g. tumors, connew angiogenesis-related nucleic acids or related polypeptides, antibodies or antisense sequences.
                                                                                                                                                                                                                                                                                                                                                                                     Claim
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DB; ADI26773.
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AL MAHMOOD S.
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RESULT 28
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Matches 103;
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The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I, ADI26740-ADI26744 and ADI26766-ADI26769) from an endothelial cell gene the expression of which is induced by an angiogenic agent, or its complement or fragment; polypeptide (II; ADI26745-ADI26749 and ADI26770-ADI26773) encoded by (I), or its fragment; an antisense nucleic acid (III; ADI26750-ADI26753) able to inhibit expression of (I); or an antibody (Ab) that binds (II). The compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; ophthalmological; Antiarthritic; Antirheumatic; Antiinflammatory; Antiarteriosclerotic; Antipsoriatic; Gynaecological; Vasotropic; Vulnerary; Hypotensive; Antianginal; Cardiant; Osteopathic; gene therapy; antiangiogenic; tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atherosclerosis; neovascularization; restenosis; cardiovascular disease; hypertension; Raynaud disease; restenosis; cardiovascular disease; hypertension; Raynaud disease;
                                                                                                                       Claim
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                                                                                                                                                 antibodies
                                                                                                                                                            Antiangiogenic composition, usefunew angiogenesis-related nucleic
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                                                                                                                                                                                                                                           Schneider
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                                                                                                                                              or antisense sequences.
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                                                                                                                       ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence,
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211. .6045
                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "CHD3"
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                      29; 110pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                           useful
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Pred. No. 0.004
0; Mismatches
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                                                                                                                       French.
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                                                                                                                                                            acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; CHD3; gene; ds.
                                                                                                                                                              treating e
or related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                            .g. tumors, co
polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6331;
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                                                                                                                                                                         comprises
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RESULT 29
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Best Local S
Matches 103
                                              contacting acid, with
                                                                                                                                                                                                                     05-JUN-2001;
10-OCT-2001;
22-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are used for treating a wide range of angiogenic diseases: tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis associated with neovascularization; restenosis (arterial or after balloon angioplasty); overgrowth of cells in wound healing; peripheral vascular disease; hypertension; vascular inflammation; Raynaud disease; aneurysm; thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chronic heart disease; (congestive) cardiac insufficiency; age-related muscular degeneration and osteoporosis. This sequence encodes CHD3.
                                                                                                                                                                                                                                                                                                                                                                               Human; p53 pathway; therapeutic; angiogenic disorder; apoptotic disorder; chromodomain helicase DNA binding protein; CHD; cancer; gene therapy; cell proliferative disorder; chromatin organisation modifier domain;
                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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                     Disclosure; Page 51-54;
                                                         Identifying a candidate p53 pathway-modulating targets for disorders related to defective p53 contacting an assay system having purified CHD
                                                                                                                                                 Friedman
                                                                                                                                                                                               15-FEB-2002;
15-FEB-2002;
                                                                                                                                                                                                                                                                        03-JUN-2002; 2002WO-US017466
                                                                                                                                                                                                                                                                                                                        WO200298899-A2
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       cytostatic;
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nilarity 58.9%;
Conservative
                                               a test
                                                                                                                                                                                            ; 2001US-0296076P.
; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
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                     278pp;
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Pred. No. 0.00
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72;
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                                                         agent as therapeutic function e.g. cancer polypeptide or nucle:
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                                                             cancer by r nucleic
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RESULT 30
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Best Local Simi
Matches 103;
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                                                                                                                                                                                                                                                                                                                                                                       gene therapy; antiangiogenic; tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atherosclerosis; neovascularization; ovarian hyperstimulation; psoriasis; endometriosis; neovascularization; restenosis; cardiovascular disease; hypertension; Raynaud disease; muscular degeneration; osteoporosis; human; zing finger; helicase; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiinflammatory; Antiarteriosclerotic; Antipsoriatic; Gynaecological; Vasotropic; Vulnerary; Hypotensive; Antianginal; Cardiant; Osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; ophthalmological; Antiarthritic; Antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GS-N3
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                                                                                                                                                                                                                                                                                                                              Homo
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                                             Colin S,
                                                                                                                         22-MAR-2002; 2002FR-00003655
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2003-806304/76
DB; ADI26747.
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                                                                          GENE SIGNAL.
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No. 0.0048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
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RESULT 31
ABX63370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I; ADI26740+ADI26744 and ADI26766-ADI26769) from conference of: nucleic acid (I; ADI26740+ADI26744 is induced by an anticomposition of the expression of which is induced by an angiogenic agent, or its complement or fragment; polypeptide (II; ADI26745-ADI26749 and ADI26770-ADI26773) encoded by (I), or its fragment; an antistense nucleic acid (III; ADI26750-ADI26733) able to inhibit expression of (I); or an antibody (Ab) that binds (II). The compositions are used for treating a wide range of angiogenic diseases: tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atherosciecrosis; ovarian hyperstimulation; psoriasis; endometriosis associated with neovascularization; restenosis (arterial or after ballon angioplasty); overgrowth of cells in wound healing; peripheral vascular disease; hypertension; vascular inflammation; Raynaud disease; aneurysm; thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chronic heart disease; (congestive) cardiac insufficiency; age-related muscular degeneration and osteoporosis. GS-N3 encodes a zing finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                          gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antiangiogenic composition, useful for
new angiogenesis-related nucleic acids
antibodies or antisense sequences.
                                 28-JUL-2000; 2000US-0222469P.
08-JAN-2001; 2001US-0260483P.
                                                                                                                                                                                                                                                                                                                     Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
                                                                                                                                                                                                                                                                                                                                                        Human cDNA #370 differentially expressed in activated vascular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX63370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX63370 standard;
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                                                                                          08-JAN-2002; 2002US-00044090
                                                                                                                                26-SEP-2002.
                                                                                                                                                                   US2002137081-A1
                                                                                                                                                                                                                                                                                                   hypotensive; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA; 7805
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                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                   gynaecological; vasotropic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 1273 T; 0 U; 0
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Best Local Sim
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 connection a sample, or screening several molecules or compounds to dentify a molecule or compound that specifically binds a cDNA of the conversal invention. A protein encoded by the cDNA may be used to screen several conversal molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for CC diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery CC disease, hypertension, diabetes, pre-eclampsia, ischaemia - reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue. Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081
hepatotropic; antiinflammatory; virucide; cytostatic; gene t differentially gene expression; liver; toxin; liver disorder biliary cirrhosis; X-linked adrenoleukodystrophy; Zellweger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiarteriosclerotic; cytostatic; cardiant, hypotensive; antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more compared.
                                                                                           Human liver differentially expressed cDNA seq id 400
                                                                                                                                                 22-APR-2004
                                                                                                                                                                                                                                        ADI22590 standard; DNA; 7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7805 BP; 2003 A; 1945 C; 2323 G; 1534 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises several cDNAs that are differentially expressed in activated vascular tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGACGAGTGTGCCGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                       GCTGCCCTCACTGTGAGAAGGAGGGGGGGTCCAGTGGGAGGCCCAAGGAAGAAGA 1804
                                                                                                                                                                                                                                                                                                                                                                                                GGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
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                                                                                                                                              (first
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                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Length 7805;
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                        c; gene therapy;
disorder;
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WO2003000898-A1

Oryza sativa

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RESULT 33
ADA71938/c
ID ADA719
XX ADA719
XX ADA719
XX CO-NOV
XX ZO-NOV
XX Rice g
XX Plant;
XX gene;
XX gene;
XX Gryza
XX Oryza
XX NO2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 103;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7805 BP;
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                                                                                                                         Plant; bacterial
                                                                                                                                                                    Rice gene,
                                                                                                                                                                                                                                                                       ADA71938;
                                                                                                                                                                                                                                                                                                                    ADA71938 standard;
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                                                                                                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000; 2000US-0251986P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1690
                                                                                                     ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                         SEQ ID 5263
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                                                                                                                                                                                                                       (first entry)
                                                                                                                            infection;
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                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                         fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59.8;
Pred. No. 0.
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                                                                                                                            viral infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang H,
Katagiri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001; 2001WO-IB001105
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246
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                                                                                                                                                                                                                                                                                                                                                                             MTCTMYTSMKGSTRRSKWGRWSGMSRMYMRWWKKMRKRKYMRYMKWKCTWRRCMCYRWGY
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                                                                                                                                                                                                                   TGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGC
                                                                                                                                                                                                                                                    CCYAMCWKAAYSGMMMYWYRKYSKWMRMSTKYMWSMW----YKKCRSMKYGAKGCYGCK
                                                                                                                                                                                                                                                                                 CCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGCGTTGCGGGG
                                                                                                                                                                                                                                                                                                                                              ACCTGCCGGCTCCGCCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                             AGGTAAGAGGTCCACCTGGGGAACCCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                            SCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGK
WSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYCGCSYCGSSKWKYMSKSCSM
                            CCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACC
                                                                                           KYWYKRRGTMSWYGKSYKKKYCTWWCYMKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYW
                                                                                                                                                                                       MWTYCSYGYMKWYTYMGSYKYSRCYKYMR-MYMYKGWMYMMYYSAYSSMMTWYYYYAKYW
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F, Quan
                                                             CCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338; Mismatches 290;
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Pred. No. 0
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                                                                                                                                        The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
diseases, pulmonary vasoconstriction, inflammation, allergic risk acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmon disease (COPD), and cancers such as leukemias, lymphomas, carcino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; colon cancer; breast cancer; lung cancer; pancreatic cancer;
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09-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 37;
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hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6124 BP; 1706 A; 1562 C; 1509 G; 1347 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 21665;
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genes from Drosophila and
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11-JUL-2000;
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                                                                                                                                                                                                                                                  AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
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            TGGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTG
                                                                                                                       ccreegectriccaccreectreccrerccccccccaeaaaarccccaeregaacc
                                                                                                                                                                                           AACGAGGACTGGTGCGCCGTCTGTCTGGATGGAGGCGAGCTGATGTGCTGCGACAAGTGT
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                                                                                                                                                                                                                                                                                                               Conservative
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2000US-00614150.
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ABL09060
                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-BBL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                               Sequence 21747 BP; 6181 A; 4697 C; 4637 G; 6232 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 21662; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE
                                                                                                                                                                                                                Local Similarity
                                                                                                                                17810
                                648
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)B; ABB64957.
                                                                                                                                                                 528
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                                                                                                                                                     AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGAGCTCATCTGCTGTGACGGCTGC 587
GAGAGCTGGCAGTGCCTACTGTGCGTCAACATCAAGGAGCTG
                               TGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTG
                                                              CCCAAAGTTTTCCATCAGAACTGTCACATCCCTGCGATCAGCTCGTTGCCGGACGAGAGC
                                                                                   CTTCGGGCCTTCCACCTGGCCTGCCTGCCTCCGCTCCGGGAGATCCCCCAGTGGGACC
                                                                                                                                AACGAGGACTGGTGCGCCGTCTGTCTGGATGGAGGCGAGCTGATGTGCTGCGACAAGTGT 1786
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                                                                                                                                                                                                  Conservative
                                                                                                                                                                                             3.7%; Score 56.4; DB
59.3%; Pred. No. 0.03;
ative 0; Mismatches
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                                                                                                                                                                                                66;
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8X5

ACH90409;

Query Match Best Local Similarity

3.6%;

Score 55.4; Pred. No. 0.

Length 153;

153

BP; 29

A; 48 C;

43 G; 33

T; 0 U; 0 Other, DB 12; .025;

ACH90409/c RESULT 37

ACH90409 standard; DNA; 153 BP

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The invention relates to a nucleic acid probe for measuring human gene cexpression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and concoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that thybridises under high stringency conditions to a nucleic acid molecule cexpressed in human cells or tissues. Also included are a spatially-cardiage expression (comprising a plurality of single exon nucleic acid molecule card addressable set of single exon nucleic acid molecule acid gene expression (comprising a plurality of single exon nucleic acid molecule contiguous and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a wector comprising the single exon probe cited above, an ORP-encoded peptide comprising the single exon probe cited above, an ORP-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an construction of a customer desiring to measure gene expression, a method of providing the man gene expression data by subscription, and a computer-readable carded above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying cated above. The probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross smaller genomic alterations, in priming the synthesis of nucleic acids, cor in expressing the ORP-encoded peptide. The present sequence is a human caids. The probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising caids, cor in expressing the ORP-encoded peptide. The present sequence is a human caids. The probes of the probes of the synthesis of nucleic acids, cor in expressing the ORP-encoded pept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; probe; s8; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                    seqdata.uspto.gov/sequence.html?DocID=20030194704
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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           CC sequences in the specification, or their complements or fragments, and CC encoding at least 8 amino acids of any of the 6888 amino acid sequences (C fully defined in the specification. The probe is a single exon probe that CC hybridises under high stringency conditions to a nucleic acid molecule CC expressed in human cells or tissues. Also included are a spatially-CC addressable set of single exon nucleic acid probes for measuring human CC gene expression (comprising a plurality of single exon mucleic acid probes cited above, where each of the plurality of probes is separately CC and addressably isolatable or amplifiable from the plurality), a single CC exon microarray for measuring human gene expression, a method of CC exon microarray for measuring human gene expression, a method of CC contiguous amino acids of any of the above- mentioned amino acid conservative amino acid substitutions), an CC isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to conservative desiring to measure gene expression, a method of providing the sund of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; probe alternative
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid probe for measuring human expression, comprising any of the 27,400 fully defined nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15;
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(HANZ/)
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    gene expression data by subscription,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) PENN S G.
) RANK D R.
) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe; ss; gene expression; single exon probe; microarray;
ative splicing event; genomic alteration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 9904; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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    computer-readable
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RESULT 39
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Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 559 BP; 145 A; 163 C; 128 G; 123 T; 0 U; 0 Other;
                                                                                                    New isolated polynucleotide and encoded polypeptides, udiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and the state of the state
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23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene
food supplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS82330;
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                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
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                                                                                 biodiversity.
                                                                                                                                                                                                                             P-PSDB;
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                                                                                                                                                                                                                                ABG18143.
                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                gene mapping, identification of mutation disorders or other traits and to assess
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Pred. No. 0.
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Claim 1; SEQ ID NO 18134; 103pp; English

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AAS74874
ID AAS7
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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New isolated polynucleotide and encoded polypeptides, useful in
                                                         P-PSDB; ABG10687.
                                                                                   WPI; 2001-639362/73
                                                                                                                                                                                             (HYSE-) HYSEQ
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                                                                                                                                    Liu C,
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                                                                                                                                      Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cand in recombinant production of (II). The polymucleotides are also used comes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is considered the polymers of the polymers of quantitating a construction of the polymers of quantitating a considered to the polymers of the polymers of quantitating a considered to the polymers of quantitating and considered to the polymers of quantitating and considered to the polymers of quantitating and considered to the polymers of quantitation and as a food considered to polymers of quantitation of the polymers of the printed specification of mutations of the polymers of the printed specification, but was obtained in considered to the invention. Note: The sequence data for this considered the polymers of the printed specification, but was obtained in considered the polymers of the printed specification.
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Best Local
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer, cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK71358 standard; DNA; 37314 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7132 BP; 1723 A; 1875 C; 1964 G; 1569 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 10678; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity.
                                                                                                               17-JAN-2001; 2001WO-US001354
                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                          WO200157182-A2
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                                                                                                                                                                                                                                                                                                                      immune/haematopoietic antigen genomic sequence SEQ ID NO:26170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
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; 2000US-0180628P.
; 2000US-0184664P.
; 2000US-0186350P.
; 2000US-0189874P.
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
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13-OCT 2000
20-OCT 2000
20-NOV 2000
20-NOV 2000
20-OCT 2000
20-NOV 2000
20-NOV
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useful f
AAK54951 to AAK64702 amino acid sequences activity, and can be
                                                                                                                                                           WPI;
                                                                    Disclosure;
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                                                                                                     acids encoding for preventing,
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2000US-0241951P
2000US-0241785P
2000US-0241808P
2000US-0241808P
2000US-0246477P
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2000US-025929P
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encode the human immune/haematopoietic antigen (I) given in AAM82170 to AAM91921. (I) have cytostatic used in gene therapy and vaccine production. (I)
                                                                                                                                                                                                                                SCI
                                                                    26170; 3071pp + Sequence Listing;
                                                                                                     human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                            Ruben
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antigen cancers

polypeptides, and metastasis.

English.

2000US-0190076P.
2000US-020551BP.
2000US-0216647P.
2000US-0216647P.
2000US-02116880P.
2000US-021748F.
2000US-021748F.
2000US-021748F.
2000US-021748F.
2000US-02255119P.
2000US-0225511P.
2000US-0225511P.
2000US-0225757P.
2000US-0225758P.
2000US-0225768P.
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2000US-0225768P.
2000US-0231141P.
2000US-0231141P.
2000US-0231141P.
2000US-0231411P.
2000US-0

27-JUN-2000
28-JUN-2000
30-JUN-2000
30-JUN-2000
31-JUN-2000
11-JUL-2000
11-JUL

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RESULT 42
ABQ88207/c
ID ABQ882
XX ABQ882
XX ABQ882
XX Human
XX Human
XX Homo 8
XX OS Homo 8
XX WO2002
XX WO2002
XX IB-DEC
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Best Local S
Matches 86
                                                                                                                                   Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000US-0255882P.
24-APR-2001; 2001US-0285691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human osteoblast differentiation related cDNA SEQ ID NO 114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the protein acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-drived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2002
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                                                                                                                                                                                                                                                                                          WPI; 2002-557663/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMBLE CO
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                                                                                                                                                                                                                                                                                                                                                                                                   Cook JS,
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                                                                                                                                                                                                                                                                                                                                                                                                Jaiswal N,
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Claim 1; SEQ ID NO 114; 78pp + Sequence Listing; English

15-OCT-1999;

(GEMY) GENETICS INST INC

98US-0104436P 99WO-US024206. WO200021991-A1

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RESULT 43
AAA45365
ID AAA45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The invention relates to genes and their expression profiles are used CC for: (a) screening modulators of precursor stem cell differentiation into CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal CC deposition of bone tissue, abnormal rate of osteoblast formation or CC cited in (b), or monitoring the progression of bone tissue deposition. CC specific conditions include postmenopausal osteoporosis, glucocorticoid CC specific conditions include postmenopausal osteoporosis, glucocorticoid CC induced abnormalities in bone formation or bone loss, conditions that CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome CC of throus dysplasia. The present sequence is that of an osteoblast CC differentiation associated cDNA marker of the invention. Note: The CC sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO or at fern wino, intrinhihiched not segmences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoletic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autolmmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
                                                                                                                                                                                                                                                                   lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mouse; chicken; rat; secreted expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 172570 BP; 45194 A; 43991 C; 41126 G; 42258 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse secreted expressed sequence tag SEQ ID NO:1940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA45365 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGCTCCAGCTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCCCACACTGCGTG 157294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCTTCCACCTGGCCTGTCCCCTTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                         Crohn's disease; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 172570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 44
ACH48320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antivivral; antiinflammatory; cytostatic; antibacterial; antifungal; antivivral; antidiabetic; antiasthmatic; vulnerary; antiulcer; cerebroprotective; anticonvolument; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), altergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriaesis. AAA45936 to AAA45931 represent linker variants which are given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317938/27.
                                                                                                                                                                                                                Human lung tumour cDNA #453
                                                                                                                                                                                                                                                         13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 523 BP; 134 A; 113 C; 167 G; 96 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags (8ESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 695; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders
30-JUL-2001; 2001US-00918995
                                      17-APR-2003
                                                                         US2003073623-A1
                                                                                                                                                                                                                                                                                                                                  ACH48320 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as autoimmune,
                                                                                                                                                                                                                                                                                                                                                                                                                                  306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                     ss; sequencing by hybridisation; SBH; expressed sequence tag; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCCTACCATATGGTGCCTGGACCCAGACATGGAGAAAGGCCCCCGGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTCCCCACTGTGAGAAGGAGGGGATCCAGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGACTATTGCGAGGTGTGCCAGCAAGGGGGAGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGACGAGTGTGCCGTGTCGCGGACGCCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infectious, and central nervous system disorders.
                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowman
                                                                                                                                                                                                                                                                                                                                    494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55.2;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305
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RESULT 45 ADB80995 ID ADB80

ADB80995 standard;

DNA;

3039

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168 587

647

ADB80995;

X A X E X E X E X E X A X A X

RING-SH 04-DEC-2003

complex related

DNA,

SEQ ID

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(first

entry)

RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60; Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; ts9 cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;

tsg101;

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                                                                                                                                                                                                                                                                                                            38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is useful for should be sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                            Sequence 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LABA/)
(STAC/)
(DICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide comprising any one 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001; 2001US-00918995
229
                                                                                                                                                      109
                                                                                                                                                                                                                               86;
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STACHE-CRAIN
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRMANAC R T.
                                                                                                                                                                                    AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                    ATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGTGAAAAGTGC
                                                                           CCCAAAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTTCCAAGTGGAGAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 35532; 44pp; English.
TGGATTTGCACTTTCTGCC
                                  TGGAGGTGCTCCAGCTGCC
                                                                                                           ccreaeccrrccaccraeccraccrereccreccecreeagaareccaeragaacc
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                            BP; 154 A; 101 C; 102 G; 136 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                 3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stache-Crain
                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                               Score 54.2; D
Pred. No. 0.05
0; Mismatches
247
                                  999
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                                                                                                                                                                                                                                                   .053;
                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                      Length 494;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones
                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                 Gaps
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RESULT 46
ADJ56478
ID ADJ56
XX
AC ADJ56
XX
AC ADJ56
XX
DT 06-MA
DT 06-MA
CX
DT Human
XX
Human
XX
Human
XX
Homo
XX
Homo
XX
XX
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XX
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XX
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HOMO
PN US200
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, PISK, actin, myosin, Hap60, Hap70, Hap90, STMM1, STMM2A, STMM2B, VHS-UIM, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for identifying agents having antiviral activity, and for treating viral disorders caused by retroviruses, rhabdoviruses, or filoviruses. This polymucleotide represents a DNA sequence relating to a protein comprising the RING-SH complex of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhabdoviruses,
                                                                          human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy MYCN activated cell.
                                                                                                                                   Human cDNA differentially expressed in MYCN activated cells SeqID 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3039 BP; 941 A; 738 C; 664 G; 696 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Greener T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001; 2001US-0308958P.
09-NOV-2001; 2001US-0345846P.
                                                                                                                                                                  06-MAY-2004
                                                                                                                                                                                                                             ADJ56478 standard; cDNA; 3917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003033646-A2
                 US2003119009-A1
                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 68; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2002; 2002WO-US024589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEOLOGICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                  648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                                                            AATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGTGAAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGAGGACGAGTGTGCCGTGTGTCGGGAACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
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                                                                                                                                                                                                                                                                                                                                  recaecrecrecaecrece 666
                                                                                                                                                                                                                                                                                                                                                                CCCAMAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCAAGTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                 (first
                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.2; DB Pred. No. 0.068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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                                                                                      gene therapy; ss.
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Human; full length

cDNA; cDNA synthesis; oligo-capping;

88

Homo sapiens

Human

full-length cDNA,

SEQ ID NO:

4044.

06-NOV-2001 AAK94864;

(first

entry)

AAK94864 standard;

CDNA; 3997

2478

647

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Query Match
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Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                           expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protonocogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been betained in electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the concerns of the cancers.
                                                                                                                                                                                                                                                                                                                    Sequence 3917 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PLON/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-2001; 2001US-0270784P
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                                                                                                                                                                                                                                                                                                                                                         ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.
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                                                                                                                                                                                                                                                                                                                                                                              printed specification but has been obtained in electronic format US Patent Office at
2479
                                                                            2419
                                                                                                                                                         2359
                                                                                                                                                                                              528 AATGAGGACGAGTGTGCCGTGTCTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                   66;
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NUCHTERN J C
PLON S E.
SHOHET J M.
                                                                                                                                                                                                                                                          Similarity
                                                                                                                 CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACC
                                                                                                                                                         ATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGTGAAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 284;
TGGATTTGCACTTTCTGCC 2497
                                     TGGAGGTGCTCCAGCTGCC 666
                                                                            CCCAAAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCAAGTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuchtern JG,
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                        3.5%;
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                                                                                                                                                                                                                                                        Score 54.2; DB 10;
Pred. No. 0.071;
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RESULT 48
ADL32011
ID ADL32
XX ADL32
XX ADL32
XX ADL32
XX Pull
DE Full
XX Auman
KW Auman
KW Oligc
XX Oligc
XX Oligc
XX Homo
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Matches 86
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the primer special sprinted specification, but was obtained in CD-ROM format directly
                           EP1396543-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1130094-A2
                                                    Homo sapiens
                                                                             oligo-capping
                                                                                                                   Full length human
                                                                                                                                               20-MAY-2004
                                                                                                                                                                                                  ADL32011 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing
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 10-MAR-2004
                                                                                         human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic manipulation.
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                                                                                                                                                                                                                                                                                                                                              CTTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACC
                                                                                                                                                                                                                                                                                                                                                                        AATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGTGAAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4044;
                                                                                                                                                                                                                                                                                                                     CCCAAAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCAAGTGGAGAG
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2000JP-00118774
2000JP-00183765
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                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 1221 A; 944 C; 911 G;
                                                                              method; ss;
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                                                                                                                   cDNA clone
                                                                                                                                                                                                  cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5%;
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a T, Nagai
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                                                                              gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54.2;
Pred. No. 0
                                                                                                                   SeqID 4044.
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K, Kojima
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S, Otsuki
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. T, Koga
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RESULT 49
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rength cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                      pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; colon cancer; barcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                       Antisense oligonucleotide; multiple target; antisense treatm impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T,
             Synthetic
                                                                                                            acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                    Human adenosine Al receptor antisense oligonucleotide
                                                                                                                                                                                                                                                                                       AAX53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotide primers length human cDNAs.
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                                          prostate cancer;
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DB; ADL32012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGAGGACGAGTGTGCCGTGTCTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGAAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                TGGATTTGCACTTTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                            TGGAGGTGCTCCAGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAAAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCAAGTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 99JP-00194486.
; 2000JP-00118774.
; 2000JP-00183865.
; 2000EP-00114089.
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                                                                                                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.5%;
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na T, Nagai
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Pred. No. 0.07:
0; Mismatches
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K, Kojima
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3, Otsuki
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                                                                                                                                                                                                  fragment.
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directed against at least 2 mRNAs selected from target genes, coding and C non-coding regions of RNAs corresponding to target genes, gene initiation CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3' CC -end and the juxta-section between coding and non-coding regions and all C segments of RNAs encoding proteins associated with one or more diseases, CC conditions or mixtures. The antisense oligonucleotides may be derived CC from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of C diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung CC diseases, pulmonary vasoconstriction, inflammation, respiratory CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension, cc pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. C colon cancer, breast cancer, lung cancer, melanoma, hepatic metastases, as the lungs of cancers which may metastasize or have metastasized for the lungs of cancers which may metastasize or have metastasized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides used in treatment of, e.g. pulmonary
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                                                                                                                                                                                                                                                                                                                                         GGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGGGGTTGCGGGGGTGTGCGGAGATGGT
                                                       GGGCCGAGCCAGGGGCCCNNHNINNSVGCGGAGCCVGCGCCCNNHNINNSCGGCCCGGCCNN 105480
                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTCGGGACGGCGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGC
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                                                                                                                             TGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGCACCTGCCGGCTCCGCC
                                                                                                                                                                                               CNNHNNNSCGGCCCGGCCGGCGGCGNNHNNNSCGG
                                                                                                                                                                                                                                CGTGGAGACCCCGCTCCCCCCGGGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAGGTCCACC
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98US-00093972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
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Pred. No.
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The present invention relates to human single exon nucleic acid probent (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging
                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #15023
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                                                                                                     Claim
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                                                                                                                              genome-derived single exon nucleic acid probe expression in human cervical epithelial cells.
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                                                                                                  SEQ ID NO 15023; 487pp;
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2000US-0068408.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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RESULT 52
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ID ARISOPA
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XX Probe;
XX Prob
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Matches 84; Conserv
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Best Local Similarity
Matches 84; Conserv
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26-MAY-2000; 2000US-0207456F.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEB-2000; 2000US-0234667P.
27-SEB-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                 Sequence
                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SEN The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are use for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Pred. No. 0.09;
0; Mismatches
                                                                                                                                                 67 G;
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ABA37266/c
                                                                                                                          Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-020745E9.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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                                                                                                                                                                                                                                      Sequence 292 BP; 65 A; 94 C; 67 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488899/53
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27-SEP-2000;
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                                                                                                                             84;
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                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 15732; 530pp; English.
                 ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGGAACTGCTCTGCTGTGATACCTGTC
                                                                     ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                             from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 尺
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                       61.8%;
                                                                                                                                                                                 3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
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                                                                                                                             <u>.</u>
                                                                                                                             Pred. No. 0.09
); Mismatches
                                                                                                                                                    Score 52.8; DB Pred. No. 0.098;
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                                                                                                                                                                              4.
                                                                                                                             52;
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RESULT 54
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                               Sequence 292 BP; 65 A; 94 C;
                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK44980 standard;
                                                                                                                                                                                                       the probes of the invention
                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                               Example
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                                                   589 CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCT
                                                                             140
                                                                                                    529 ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
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  GGAGGTGCTCCAGCTG 664
                           CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
                                                                           ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
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                                                                                                                                                                                                                                                                                             SEQ ID NO 19537; 658pp + Sequence Listing;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00632366
2000US-0234687P
2000US-0236359P
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2000US-0207456P
2000US-00608408
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                                                                                                                                        3.4%;
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                                                                                                                           Score 52.8; D
Pred., No. 0.09
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                                                                                                                                                                              67 G;
                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                               66 T; 0 U; 0 Other;
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                                                                                                                               52;
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                                                                                                                                                                                                                    present sequence is one of
                                                                                                                                                      Length
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                               English
                                                                                                                                                        292;
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                                                                                                                              Gaps
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RESULT 55
AAK19029/C
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ID AAK190
AC AACT
AC AAK190
AC AACT
AC AAK190
AC AACT
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RESULT 56
ABS44646/c
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
                                                                                                                                                            GGAGGTGCTCCAGCTG
                                                                                                                                                                                                                                                                                                 ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
                                                                                                                                                                                                                                                                                                                                            CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
                                                                                                                                                                                                                                               crossectrocaccrescristorercccreccrescesses
                                                                                                                  GGCTCTGTCCCCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 19020; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0207456P.; 2000US-00608408.; 2000US-00632366.; 2000US-0234687P.; 2000US-0236359P.; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 65
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                                                                                                                                                                                                                                                                                                                                                                                                            3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α,
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Pred. No. 0.09;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 G;
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                                                                                                                                                                                                                                                                                                                                                                                                               .098;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 292;
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ABS44646

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RESULT 57

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Matches 84
                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
                                                                                                                                                                                                                        Sequence 292
                                                                                                                                                                                                                                                                 sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from W
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 19636; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
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                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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                                                                                 589
                                                                                                           140 ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
20
                                                       80
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                                                                                                                                                                                Similarity
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                                                                                                                                        ATGAGGACGAGTGTGCCGTGTCGCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
                           GGAGGTGCTCCAGCTG 664
                                                                          CTCGGGCCTTCCACCTGGCCTGCCTGTCCCGCTCCGGGAGATCCCCAGTGGGACCT
                                                     CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
                                                                                                                                                                                                                        BP; 65 A; 94 C;
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2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
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                                                                                                                                                                                3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adult
                                                                                                                                                                 Score 52.8; D
Pred. No. 0.09
0; Mismatches
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                                                                                                                                                                                                                        67 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
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ABS19225/c

ID

ABS19225;

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AC

ABS19225;

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DT

19-AUG-2002 (first of the control of the c
The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of CC 12614 nucleic acid sequences mentioned in the specification, or their CC complements or the 1287 open reading frames derived from the 12614 CC probes. Also included are a microarray comprising the novel set of probes (the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample CC derived from human lung; comprising (a) contacting the array with a CC collection of detectably labeled nucleic acids derived from human lung exons in a eukaryotic genome, comprising (a) CC mRNA, and (b) measuring the label detectably bound to each probe of the carray; identifying exons in a eukaryotic genome, comprising (a) CC labeled nucleic acids from entaryote in microarray from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably classed nucleic acids from exaryote in the predicted exon, the probe is included comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the comprises on the exons in the tissues are used for gene expression one of an exonal point frames (ORF). The probes are used for gene expression one of an exonal point dentifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spatially-addressable set of single exon nucleic acid probes, used
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26-MAY-2000; 2000US-0207456P.
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familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ds; single exon probe; asthma; lung cancer; COPD; chronic obstructive pulmonary disease; interstitial lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon probe ORF from lung SEQ ID No 19216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 19216; 634pp; English.
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2000US-00632366.
2000US-0234687P.
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2000US-00024263.
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RESULT 58
AAI15873/c
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
                                                                                                                                                                                                                     WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #5806 for gene expression analysis in human cervical cell sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression;
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Pred. No. 0.09
0; Mismatches
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived

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5806;

487pp;

English

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

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RESULT 59
ABA58175/c
ID ABA581
XX ABA581
XX ABA581
XX Human
XX Human
XX Homo (
XX WO200:
XX WO200:
XX WO30-JU
PR 30-JU
PR 31-SE
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
04-OCT-2000; 2000GB-00024263.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring ar displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                        n genome-derived single exon nucleic expression in human fetal liver.
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification, but was obtained in electronic format
at ftp.wipo.int/pub/published_pct_sequences
                                            The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gexpression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                1782/c
AAI37782 standard;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                              genetic
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                              measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                          Single
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                                            Sequence
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RESULT 62
AAK31915/c
ID AAK319
XX AAK319
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                                                                                                                                                      Matches
                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P-
26-MAY-2000; 2000US-0207456P-
30-JUN-2000; 2000US-00608408-
03-AUG-2000; 2000US-00632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                    Sequence 476 BP; 131 A; 132 C; 103 G; 110 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n genome-derived single exon nucleic acid expression in human bone marrow.
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          589
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                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
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                                                          ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 6472; 658pp + Sequence
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                         Conservative
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                                                                                                                                                                             3.4%;
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                                                                                                                                                                               Score 52.8;
Pred. No. 0
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RESULT 63
AAKO6255/c
ID AAKO62
XX AAKO62
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XX Human
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KW Allzhei
KW Allzhei
KW SB;
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XX WO2001
XX O4-FEB
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Best Local S
Matches 84
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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    GGCTCTGTCCCCGTTG
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                                                                                                                                                                                                                                    crossociations and consequences of the contract of the contract
                                                                                                                                                                                                                                                                                                                   ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGGAACTGCTCTGCTGATACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                  ATGAGGACGAGTGTGCCGTGTCTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes for analyzing gene expression in
                                                                               664
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Pred. No. 0.1;
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RESULT 64
ABS31605/C
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Best Local Similarity
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 476 BP; 131 A; 132 C; 103 G; 110 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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GGAGGTGCTCCAGCTG
                                                                                                                                                                                                                                             ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                         CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCCAACGGTGAAT
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Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 476;
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GGCTCTGTCCCCGTTG 293

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The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived CC from human lung comprising single exon nucleic acid probes having one of CC 12614 nucleic acid sequences mentioned in the specification, or their CC complements or the 1287 open reading frames derived from the 12614 CC probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample CC derived from human lung, comprising the array with a CC collection of detectably labeled nucleic acids derived from human lung comprising the array with a CC array; identifying exons in a sukaryotic genome, comprising (a) CC array; identifying exons in a sukaryotic genome, comprising (a) CC the sukaryote; and (b) detecting specific hybridisation of detectably cC labeled nucleic acids from sukaryote lung mRNA, to a single exon probe, the sukaryote; and (b) detecting specific hybridisation of detectably cC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC issues and/or cell types using hybridisation to a single exon serveral crisques and/or cell types using hybridisation to a single exon for expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-020604408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; hermansky-Pudlak syndrome; sarcoidosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cyllary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-114183/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression in human lung samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6668;
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RESULT 66
ABL29649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 476 BP; 131 A; 132 C; 103 G; 110 T; 0 U; 0 Other;
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                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                    WPI; 2001-656860/75.
                                                                                                                                                                 Venter
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                                                                                                                                                                                                                                                                                                  27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 40420.
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                                                                                                                                                              PWD,
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Pred. No. 0
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent

invention

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Claim 1; SEQ ID NO 40420; 21pp + Sequence Listing; English

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell

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RESULT 67
ABL29648/c
ID ABL296
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                                                                                                                                                                                                                          New isolated nucleic a genes from Drosophila interactions.
                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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11-JUL-2000; 2000US-00614150
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No. 0.15;
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Best Local Similarity
Matches 105; Conserv
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                                                                                                                                                                                                                                                                                                                                                  haematopoletic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; inmune deficiency; inmune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiallergic; antinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antialcerial; fungicide; immunostimulant; cerebroprotective; gene therapy; gene; ss.
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                         Claim
                                               New isolated polynucleotide, useful in research, therapeutic methods, e.g. preventing or treating aberrant protein expression or biological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human coding sequence SEQ ID 202.
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disorders i
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The

present invention

relates to novel human coding sequences (ABQ99268-

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RESULT 69
ABV44220
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CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of blo-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC menufacture diseases, involving aberrant protein expression or
CC biological activity, e.g. haematopoietic disorders, central/peripheral
CC mounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic
CC reactions and conditions, coagulation disorders, or cancer. The
CC isolated mainly by sequencing by hybridisation, and in some cases,
CC sequences obtained from one or more public databases. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC from wincounty in the content of the printed specification, but
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Matches 76
                                                                                                                                     17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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   Schlegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression marker cDNA 44211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%;
                                                                          PREDICTIVE MEDICINE INC
   Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.</u>
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Pred. No. 0.16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4653;
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밁 S 밁 S

Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer.

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RESULT 70
ABV29094
ID ABV29
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Best Local
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                                                                                                                                                                              17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 29085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 539 BP; 125 A; 148 C; 150 G; 115 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                          20-FEB-2001; 2001WO-US005171
                                                                                                                                                                                                                                                                                                                     WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV29094 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-662795/76
                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553 GGGACGGCGGGAGCTCATCTGCTGTGACGGCCTGCCCTCGGGCCTTCCACCTGGCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGAACCTGGAGGTGCTCCAGCTGC 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 8783; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAMACCCTCCCCTGCCTGACATTCCCAATGGTGAATGGCTGTGTCCCCGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0183319P.
; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
; 2000US-0255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                     Endege
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%;
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                                                                                     Monahan
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Pred. No. 0.14
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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Claim 1; Page 6175; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastazed in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient in the aggressiveness or indolence of prostate cancer in a patient in a patient.

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RESULT 71
ADC30621
ID ADC30621
AC ADC30
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Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
                               New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human novel cDNA sequence,
                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                   Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-2001; 2001US-0324631P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular weight marker; food supplement; antiparkinsonian; nootropic neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC30621 standard; cDNA; 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ulcers; osteoporosis; autoimmune disease; cancer;
                                                                                                                                                                                                                            2003-371981/35.
                                                                                                                                                                                                                                                                                                                                           Ghosh
                                                                                                                                                                                                                                                                                                                                   Zhang J,
Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                       Drmanac RT;
                                                                                                                                                                                                                                                                                                                                   Ren F,
Wang D,
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                                                                                                                                                                                                                                                                                                                                       Xue AJ, Zhao
Ma Y, Asundi
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Wang Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628) are nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The observation of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1670 BP; 374 A; 596 C; 488 G; 212 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC30889) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 703; 1185pp; English
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                                                                                                                                                                                                                                                                                                                                                 ACGATGAGCACTGTGCCGCCTGCAAGCGAGGGGCCAACCTGCAGCCCTGCGGCACCTGCC
GGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAG
                                                                                                                                                                        CGGGGGCCTACCACCTCAGCTGCCTGGAGCCGCCCCTCAAGACGGCGCCCCAAGGGCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No.
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1246
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GGGACGGCGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCC

Matches Query Match Best Local :

Similarity

3.4%;

Score 52.2; Pred. No. 0.

DB

Length 539; Indels

Conservative

0;

Mismatches 0.14;

38; 5 '

0;

109 612 Sequence 539 BP; 125 A; 148 C; 147 G; 113 T; 0 U; 6 Other;

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110

TAAACCCTCCCCTGCCTGACATTCCCAATGGTGAATGGCTGTGTCCCCGATGC TGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGC 665

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Cytostatic; antiatherosclerotic; osteopathic; antiarteriosclerotic; hepatotropic; antipsoriatic; antiallergic; antianaemic; antiasthmatic; antithyroid; antiinflammatory; anthelmintic; antidiabetic; nephrotropic ophthalmological; immunosuppressive; dermatological; antiulcer; antirheumatic; antiarthritic; antibacterial; virucide; fungicide;
antirheumatic; antiarthritic; antibacterial; virucide; fungicide; antiarthritic; protozoacide; tranquillser; vulnerary; anti-HIV; antioprotoctive; anticonvulsant; cerebroprotective; neuroprotoctive; anticonvulsant; cerebroprotective; neuroleptic; molecules for disease detection and treatment; MDDT;
                                                                                                                                                                                                              MDDT related human
                                                                                                                                                                                                                                                                                                                                                          AAK99602 standard;
                                                                                                                                                                                                                                                             10-APR-2003
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                              DNA SEQ ID No
                                                                                                                                                                                                                                                                                                                                                       DNA; 1965
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nephrotropic;

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The invention relates to an isolated polypeptide chosen from molecules CC for disease detection and treatment (MDDT), comprising a one of 39 114-CC 1250 residue amino acid sequences, given in the specification, or a biologically active or immunogenic fragment of the isolated polypeptide. CC effectiveness as an agonist or antagonist of the isolated polypeptide. CC The isolated polypeptide is useful for screening a compound for CC effectiveness as an agonist or antagonist of the isolated polypeptide. CC The isolated polypeptide is also useful as an immunogen for preparing CC polypeptide and its encoding polynucleotide are useful for diagnosis, CC treatment and prevention of cancer, actinic keratosis, arteriosclerosis, CC atherosclerosis, bursitis, cirrhosis, hepatitis, poriasis, AIDS, adult respiratory distress syndrome, Addison's disease, allergies, anaemia, CC autolimune thyroiditis, Cothn's disease, autolimune haemolytic anaemia, CC autolimune thyroiditis, Cothn's disease, autolimune haemolytic anaemia, CC scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, uveitis, viral, bacterial, fungal, parasitic, CC protozoal, helminthic infections, trauma, Alzheimer's and other disease, multiple sclerosis, dementia, and other disease, multiple sclerosis, dementia, and other developmental CC disorders of the central nervous system, neuromuscular disorders, cartain and other developmental canaemia, and cher developmental canaemia, and cher and toxic movaratios.
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01-JUN-2001; 2001US-0295257P.
08-JUN-2001; 2001US-0297220P.
21-JUN-2001; 2001US-0300526P.
29-JUN-2001; 2001US-0301874P.
22-FEB-2002; 2002US-0359413P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel molecules for disease detection and treatment and polynucleotide encoding them useful for diagnosing, preventing or treating cell proliferative, autoimmune/inflammatory, neurological and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-140448/13.
P-PSDB; AAO26249.
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Zebarjadian Y,
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nervous system, neuromuscular disorders, toxic myopathies, periodic paralysis. me
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MG, Yang;
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Best Local (
                      The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
                                                                                                                                                                                                                New polynucleotides and preventions a diagnostic respression and activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders including mood, anxiety and schizophrenic disorders, anaemia, renal tubular acidosis, epilepsy, hypothyroidism, glaucoma, sensorineural hearing loss and cataract. This polynucleotide sequence represents the DNA encoding a human MDDT protein relating to the invention
                                                                                                                                                                                       Claim 1;
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Seki N, Yoshikawa
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, I
                                                                                                                                                                                                              polypeptides are useful marker or medicines for , or as a target of gene
                                                                                                                                                                                    305pp; English.
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Pred. No.
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        The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding with the antibody of the encoded protein, and observing the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related osteoporosis; neurological disease; cancer; tumour.
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                                                                                                                                                             New polynucleotides and polypeptides, useful marker or medicines for regulation of their \epsilon
                                                                                                                                                                                                                                           Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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25-JAN-2002; 2002US-00350978.
 between the two,
                                                                                                                       Claim 1;
                                                                                                                                              as targets of gene therapy.
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                                                                                                                       Page; 222pp; English.
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a transformant carrying the
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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polynucleotide
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Isogai T, Yamamoto J Seki N, Y

J, Isono Yoshikawa

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Otsuki T, Wakamatsu A, Hio Y, Otsuka K, Nagai Otsuka M, Nagahari K, I

Masuho

Sato H,

Ishii S;

Tamechika

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Sugiyama T, Isono Y,

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tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
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25-JAN-2002;
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(REAS-)
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                                                                                                                                                                                                                                                 2001JP-00379298
2002US-00350978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 679. .1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Clone FCBBF30142290 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%;
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Pred. No. 0.2;
0; Mismatches
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RESULT 76
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The oligonucleotide proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a CDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                     ADQ24519 standard; DNA; 3710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3584 BP; 770 A; 1089 C; 1030 G; 695 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ADB64354.
                                                                                                                                                                                                                                  Human soft tissue sarcoma-upregulated DNA - SEQ ID 7339.
                                                                                                                                                                                                                                                                         26-AUG-2004
                                                                                                                                                                                                                                                                                                                ADQ24519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 222pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as targets of gene therapy.
                26-NOV-2003; 2003WO-US038193
                                                         10-JUN-2004.
                                                                                             WO2004048938-A2
                                                                                                                                    Homo sapiens
                                                                                                                                                                                           soft tissue
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                                                                                                                                                                                           sarcoma;
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57.3%;
                                                                                                                                                                                             cytostatic;
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Pred. No. 0.21;
0; Mismatches
                                                                                                                                                                                           gene therapy; vaccine; screening;
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is so that of a human soft tissue sarcom vithin the specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                           Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice gene,
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                                                                                           22-JUN-2001; 2001WO-IB001105
                                                                                                                                                    22-JUN-2001;
                                                                                                                                                                                                                03-JAN-2003
                                                                                                                                                                                                                                                                            WO2003000898-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-2002; 2002US-0429739P
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                                  (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGGGGCCTACCTCAGCTGCCTGGAGCCGCCCTCAAGACGGCGCCCAAGGGCGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7339; 210pp;
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                                                                                                                                                       2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogenic inrection bacterial, fungal or gene expression.
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                                                                                                                                                                                      MGTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMSARYTMRYCARKKYSYSAARKAR
                                                                                                                                                                                                                                     ACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCAGC----CCCGCCCGCCTGGCC
                                                                                                                                                                                                                                                                                RAWKMGCRGCMTCRMKGYGMMRWKSWKRMASKYKMMSRMYRWRKKKCSRTTMWGKTRGGM
                                                                                                                                                                                                                                                                                                                                                                                                                              GAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSGRMAGGSGRMMGGKSRMSYWMWCYARGCGSCKRKKSKGGSWGKTCRRGARGGSGWSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKRSKMSAWSKSMRSSRKCRKCASKRSSAKR
                                            GAGTCCCTTCTGAGCGAGCACACCTTCGATG
                                                                                                                                      CCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTG
                                                                                                                                                                                                                                                                                                                                    ACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCCAGATCCTGCTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                              MRWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGCGCGTTGCGGGGTGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSYSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWYSWSYKMWMCTAYKKSYYSRWCYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCTCCGGCCTTCTGCAGCCCCGGCTGCCAGGTCTGGACTCCTCGGCCCTGCACCCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGCCACCCGTGGAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGGAGGAGGAGGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSAGWKSRCSSWRGRRRMYMAGMMSCARMGSSRMSRKMGSMSKYRKCSSCGKCKMTTRRK
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                                                                                         CWYRGKGYYWAGMWMKRYKRMYMYKMWWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YRGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKYKS---GSMSKRMWMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ູດ
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S, Tao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'nά
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2000;
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30-AUG-2002; 2002US-0407068P.
26-SEP-2002; 2002US-0414139P.
05-NOV-2002; 2002US-0424094P.
17-JAN-2003; 2003US-04240912P.
24-JAN-2003; 2003US-0442419P.
The present sequence encodes a human nucleic-acid associated protein designated NAAP-31. NAAP sequences have antiparkinsonian, nootropic, neuroprotective, muscular, neuroleptic, antidiabetic, antithyroid, cytostatic, dermatological, antiinflammatory, immunosuppressive, antiallergic, nephrotropic, virucide, antibacterial, fungicide, antiparasitic, protozoacide, antihelminthic, antiarteriosclerotic, cardiovascular, gastrointestinal and hepatotropic activities, and caused in gene therapy. The NAAP polypeptide or its fragments, and the polynucleotide encoding the polypeptide are useful in diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forsythe IJ, Elliott VS, Lo
Khare R, Marquis JP, Becha
Griffin JA, Lee S, Yue H,
Gera M, Gietzen KJ, Nguyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; cardiovascular; gastrointestinal; hepatotropic; gene therapy; neurodegenerative disorder; parkinson's disease; Alzheimer's disease; muscular disorder; myotonic dystrophy; catatonia endocrine disorder; diabetes; Grave's disease; cancer; leukaemia; cervical cancer; breast cancer; immunological disorder; scleroderma; systemic lupus erythematosus; allergy; gastrointestinal disorder; cordin's disease; renal disorder; Goodpasture's syndrome; infection; cardiovascular disorder; atherosclerosis; hepatic diseases; cirrhosis
                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid-associated proteins (NAAP) polypeptides, useful diagnosing, preventing and treating disorders with abnormal activ NAAP, e.g. neurological, immunological, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mason
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immunosuppressive; antiallergic; nephrotropic; virucide; a
fungicide; antiparasitic; protozoacide; antihelminthic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-2003; 2003WO-US023245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antithyroid; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Swarnakar A, ...
a IJ, Elliott VS, Lee
a IJ, Elliott VS, Lee
Marquis JP, Becha SD, beche S, Yue H, Yang YC
Tee S, Yue H, Yang YC
T. Nguyen DB, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCYTE
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                                                                                                                                                                                                                                                                                                        SEQ
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                                                                                                                                                                                                                                                                                                        IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "nucleic-acid associated protein NAAP-31"
                                                                                                                                                                                                                                                                                                        66;
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                                                                                                                                                                                                                                                                                                     290pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X, Jackson AA, Kable AE, SY, Lee EA, Ison CH, Ha, DD, Bulloch SA, Blake JJ, ang YG, Sprague WW, Baughn B, Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baughn
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Best Local S
Matches 71
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                                                                                                                                                                                              length cDN
diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:15067.
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises
(a) an oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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27-AUG-1999;
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                                                                                                                Claim
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                                                                                                                8
                                                                                                                                                                                     sets for synthesizing polynucleotides, particularly the 5602 full-
cONAs defined in the specification, and for the detection and/or
sis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer;
                                                                                                                                                                                                                                                                                                                                                         Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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99JP-00300253.
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                                                                                                       15067; 2537pp +
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Pred. No. 0.93;
0; Mismatches
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A, Nagai K,
                                                                                                             Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                            Saito K,
C, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto
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                         comprises:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc complementary strand of a polynucleotide which comprises one of the 5602 cnucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination cf an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a combination of sequence and an oligonucleotide comprising a sequence complementary to a colynucleotide which comprises a 3'-end sequence complementary to a colynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in cg gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH19528 and CC cDNAs easily without any specialised methods. AAH03166 to AAH19528 and coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 71
                                                                                                   19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                              03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                        WO200157190-A2
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK52998
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           y, Zhao QA, 'AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 CCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 65.771; Conservative
                                                                        HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGCGACACTTGTTCAAGAGTCTTCCATGAGGACTGCCACATCCCACC
                                                                                                   2000US-00620325.
2000US-00654936.
2000US-00663561.
2000US-00693325.
2000US-00728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                              2000US-00560875.
2000US-00598075.
                                                                                                                                                                                                              2000US-00496914
           Wang D, Wang Wejhrman T,
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Pred. No. 0
            Asundi V,
JJ, Zhang
Goodrich R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 97;
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                                           Zhou P,
                            Ren F,
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                            ,<del>7</del>
                                           Cao
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                           Wang ZW;
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RESULT 81
AAK52014
ID AAK52
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Best Local Similarity
Matches 108; Conserv
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis, tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 4806-4807; 6221pp; English.
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                               05-FEB-2001;
                                                                                                                              09-AUG-2001
                                                                                                                                                           WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                 AAK52014 standard; cDNA; 2179
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                                                                                                                                                                                                                                                                                                     polynucleotide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCTTAAGCACCCGGCCACCAAGGACCTGGCGGCGCAGCCGCACAGGGGCCCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACCCGTGGAGACCCCGCTCCCCCCG
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                  2000US-00560875.
2000US-00598075.
2000US-00620325.
                                                                                               2001WO-US004098.
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                               2000US-00496914.
                                                                                                                                                                                                                        disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.1%;
                                                                                                                                                                                                                        arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                        inflammation;
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                                                                                                                                                                                                                                                                    gene therapy;
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Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
Ma Y,
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2022-2024; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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P-PSDB; AAM78881.
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/, Zhao QA, 1
AJ, Yang Y,
 271
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                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                       2179
                                                                               TGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAAGGAGGCCCCCGGCCCCAGGAG
                                                                                                                     GCCGCCCGCCAGCTCAAGCGCAGCCACGTGCTCCCCCGAGGGCCGCTCGCCCCGGGCCCCCG
                                                                                                                                                                                                     GCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCCTTGCCGCCTTCCAC
                            CCACCCGTGGAGACCCCGCTCCCCCG 749
                                                          GCCCTTAAGCACCCGGCCACCAAGGACCTGGCGGCGGCAGCCGCACAGGGGCCCCAGCTG
                                                                                                                                                CTGGCCTGCCTGCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGC
                                                                                                                                                                                GCCGTGTGTCGCGGCTGCGTGAACTTCGAGGGCGCGCGGACCGCATCGAACTGCTCATCGAT
 CCGCCCCCCAGCCCAGCCCAGCCG
                                                                                                                                                                                                                                            Conservative
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, Wejhrman
                                                                                                                                                                                                                                                                                                       358 A; 757 C; 689 G; 375 T; 0 U; 0 Other;
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lang D, Wang
                                                                                                                                                                                                                                                      3.1%; 52.2%;
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                                                                                                                                                                                                                                                         Score 48.6;
Pred. No. 1;
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J, Zhang
Goodrich R
                                                                                                                                                                                                                                           Mismatches
297
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                                                                                                                                                                                                                                           99;
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70
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RESULT 82
ADO35478/c
ID ADO35478;

XX
AC ADO35478;

XX

BY
AC ADO35478;

XX

AC ADO35478;

XX

BY

AC ADO35478;

XX

AC ADO35478;

XX

BY

AC ADO35478;

AC
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inflammation; bacterial disorder;

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RESULT 83
AAS75442
ID AAS75
XX AAS75
AC AAS75
DT 13-PE
XX DNA 6
XX Human
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Matches 135;
                                                                                                                                                                                                                                                                                                                                             Query Match
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05-DEC-2002;
05-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                               Sequence 3005 BP; 782 A; 632 C; 849 G; 742 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises 744 novel mouse DNA sequences (genes). The DNA sequences of the invention are useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischaemic heart disease, thrombosis, immune disorders, bacterial disorders and viral disorders. The present nucleic acid represents a mouse DNA sequence of the invention. NOTE: The present DNA sequence is not shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mouse nucleic acid molecules and polypeptides, useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischemic heart disease or thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 151; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-2004
Human; chromosome mapping; gene mapping; gene therapy;
                    DNA encoding novel human diagnostic protein #11246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-2003;
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                                        13-FEB-2002
                                                                             AAS75442 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FIVE-) FIVE
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                     1190
                                                                                                                                               1250
                                                                                                                                                                                                                            1130
                                                                                                                                                                                                                                                                                                       1010 GCGCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCTGCAGATCCTG
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                                                                                                                                                                                                                                                                CATGGCCCGTCCGGCGGCCCCCTTCCCCTCCTGACCCCAG
                                                                                                                                                                                     CCTGGAGTCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAG
                                                                                                                                                                                                                          GGCCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGA 1189
                                                                                                                                                                                                                                               GCTGGGTGACGAAAGCTCTCCCGCTGGCGGCCCGGACGCTCCTCTAAGCCGAGCCCGGCA
                                                                                                                                                                   GAGCCGCCATGTCGGTGCGCCCACCCGTCGCTGCGGCTCGGGGCCCGCGGTCGCCGCCGG
                                                                                                                             CCTCGCGCGTCTGGGAGCTCGCCGTGTCCCCTCAGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0431445P
2002US-0431606P
2003US-047662LP
2003US-0476632P
2003US-0485217P
2003US-0485217P
2003US-0493332P
2003US-0493332P
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003WO-US033948
                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chu K,
                                                                                                                                                                                                                                                                                                                                  3.1%;
48.2%;
                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee
                                                                             924
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                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                        Score 48; DB 12; I
Pred. No. 1.4;
D; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hestir K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC.
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                                                                                                                                                                                                                                                                                                                                            Length 3005;
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                                                                                                                                               1289
  forensic;
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 RESULT 84
AAH33830
ID AAH33
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AC AAH33
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DT 03-SE
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DE Humar
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CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cand in recombinant production of (II). The polynucleotides are also used comes. (I) is useful in gene therapy techniques to restore normal comestuity of (II) or to treat disease states involving (II). (II) is consequence therapy techniques to restore normal complexity of (II) or to treat disease states involving (II). (II) is consequence, as molecular weight markers and as a food consequence, as molecular weight markers and as a food consequence supplement. (II) and its binding partners are useful in medical imaging consists expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The college of the polynucleotide sequences have applications in consiste for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and consists equences of the invention. Note: The sequence data for this content did not appear in the printed specification, but was obtained in cleartronic format directly from WIPO at first wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assebiodiversity.
                                                                                                                                                                                                                                                                                                                                                               Sequence 924 BP; 259 A; 192 C; 264 G; 209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 11246; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac
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                                                                                                                                                       524 GAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGG
                                                      584 CTGCCCTCGGCCTTCCACCTGGCCTGTCCCCTCC 622
                                                                                                                    51
                                                                                                                                                                                                                                           67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEQ INC.
                                                                                                                                                                                                                                                                           Similarity
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TTGTTCAAGAGTCTTCCATGAGGACTGCCACATCCCACC
                                                                                                                    GAGAAACTTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTGTTGCGACAC
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                              3.1%;
67.7%;
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Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                  Length 924;
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                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                           Gaps
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Human colon cancer antigen encoding cDNA SEQ ID NO:886

03-SEP-2001

(first entry)

AAH33830 standard;

CDNA; 1006

BP

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RESULT 85
AAH16455
ID AAH16
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AC AAH16
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression by rectifying mutations or deletions in a patient with declarate that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200122920-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1006 BP; 339 A; 191 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-US026524.
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                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-235357/24.
                                               AAH16455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                              AAH16455 standard;
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                                                                                                                                                                353
                                                                                                                                                                                               648
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                                                                                                                                                                                                                                                              588
                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                    CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCAGATCCCCAGTGGGACC
                                                                                                                                                                                                                                                                                                                          AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                               TGGAGGTGCTC 658
                                                                                                                                                                                                                               CCAAAGGTCTTTCATCTAACTTGTCATGTTCCAACACTACTTAGCTTTCCAAGTGGGGAC
                                                                                                                                                                                                                                                                                              AATGAAGACTGGTGTGCTGTCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                                                                                                                                                                TGGATATGCAC
                                                                                                                                                                                                                                                                                                                                                              Conservative
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0157137P
99US-0163280P
                                                                              cDNA;
                                                                                                                                                                                                                                                                                                                                                                           3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4277 human
diagnosing
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                                                                              2724
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Pred. No. 1.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             232 G; 239 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer-associated polypeptides,
and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen
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                                                                                                                                                                                                                                                                                                                                                                                              BB
                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                            4; Length 1006;
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                                                                                                                                                                                                                                                                                                                           587
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                                                                                                                                                                                                                                                                                                                                                                         of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end complementary strand of a polynuclectide which comprises a 5'-end complementary to a polynucleotide which comprises a 1'-end sequence complementary to a complementary 
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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02-MAY-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence SEQ ID NO:15457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HELI-)
                                                                                                                                        1953
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    648
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                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                              invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
    TGGAGGTGCTC
                                              CCAAAGGTCTTTCATCTAACTTGTCATGTTCCAACACTACTTAGCTTTCCAAGTGGGGAC
                                                                                        ccreegectriccaccreectreccretccccreegeagarccccagreegacc
                                                                                                                                      AATGAAGACTGGTGTGTGTGTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                                                                                                                                                                                2724 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 15457; 2537pp + Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-00300253
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T, Wakama
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Wakamatsu
                                                                                                                                                                                                                                                                                                                    602
                                                                                                                                                                                                                                          Score 47.8; DB
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                                                                                                                                                                                                                         Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                 C; 590 G;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                    627 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                          DB
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C, Otsuki
                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                     Length 2724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a primer set comprises:
                                                                                                                                                                                                                                Indels
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                                                     2072
                                                                                                                                           2012
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TGGATATGCAC 2083

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RESULT 86
ADP13566
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                                                                                                                                             The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having conn-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample is a whole blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples to sample is a whole blood sample (claimed). (M2) are development or treatment of RCC and/or other solid tumors. This sequence corresponds to a gene that differentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification but was obtained from WIPO in electronic format at
                                                           Query Match
Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Twine
Sloni
                                                                                                                       Sequence 3424 BP; 1029 A; 811 C; 843 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-460799/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004048933-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP13566 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2002; 2002US-0427982P.
03-APR-2003; 2003US-0459782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2003; 2003WO-US037481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TREP/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) BURCZYNSKI M
) TREPICCHIO W
) DORNER A.
) STOVER J A.
) SLONI D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WYETH.
                                                                          Similarity
AATGAAGACTGGTGTGCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                          AATGAGGACGAGTGTGCCGTGTGTCGGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burczynski
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 302; 350pp; English
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                         3.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trepicchio WL,
                                                          <u>.</u>.
                                                          Score 47.8; D
Pred. No. 1.6;
0; Mismatches
                                                                                                                       741 T; 0 U; 0 Other;
                                                                                        DB 12;
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                                                        52;
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                                                                                        Length
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                                                           Indels
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                                                          0,
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중 유

2740 AATGAAGACTGGTGCTGCCTGCCAAAACGGAGAGATCTCTTGTGCTGCGAAAAATGT 2799

AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC

588 CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCCAGTGGGACC

647

587

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RESULT 87
ADB80496
ID ADB80
XX ADB80
XX ADB80
XX ADB80
XX ADB80
XX ADB80
XX RING-
XX RING-
XX RING-
XX H8p71
KW Culli
KW FF 31-JI
PF 31-JI
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  Query Match
Best Local S
Matches 79
                                                                                                                                                            The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A, STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for dentifying agents having antiviral activity, and for treating viral disorders caused by retroviruses, rhabdoviruses, or filoviruses. This polymucleotide represents a DNA sequence relating to a protein comprising the RING-SH complex of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhabdoviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60; Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsgcullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greener T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2001; 2001US-0308958P
09-NOV-2001; 2001US-0345846P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 69; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2002; 2002WO-US024589
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                                Similarity
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                                                                                                                      3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGGTGCTC
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  Conservative
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                                                                                                                   BP;
                                                                                                                   1044 A; 832 C;
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  0;
Score 47.8; DE Pred. No. 1.6; 0; Mismatches
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                                                                                                                886 G;
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                                                     Length 3510;
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RESULT 88
ADL22564
ID ADL225AX
AC ADL22
XX
AC ADL22
XX
DT 20-MA
XX
DE Human
XX
Cell
XX
Homo
CC (INC)
XX
Homo
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                                                                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated disease detection and treatment (MDDT) DNA polynucleotide. The polynucleotide of the invention demonstrates antiarteriosclerotic, antipsoriatic and cytostatic activities and may be useful in a composition for detecting the expression of a disease detection and treatment molecule polynucleotide. The molecules of the invention may be utilised to diagnose or treat conditions, diseases or disorders associated with cell signalling, such as arteriosclerosis, psoriasis and cancer. The current sequence is that of a human MDDT cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL22564 standard; cDNA; 6730
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease detection; MDDT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human disease detection and treatment (MDDT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13; 411pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GE, Jackson JL;
Yu JY, Tuason O, Yap PE, Amshey SR, Dam TC, Liu TF, Gerstin
Peralta CH, Lewis SA, Chen AJ, Marwaha R, Lan RY, Urashka ME;
Kristnam SR, Kolluru V, Panesar IS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-2002; 2002US-0349413P
17-JAN-2002; 2002US-0349946P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-2003; 2003WO-US001363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003062379-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arteriosclerosis, psoriasis, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated disease detection and treatment diagnosing or treating conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ADL22668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS INC.
                                            1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2860
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  648
                                                                                                                                                            528 AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                         79;
                                                                                                                                                                                                                                                Similarity
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                                            CCAAAGGTCTTTCATCTAACTTGTCATGTTCCAACACTACTTAGCTTTCCAAGTGGGGAC
                                                                                      CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACC
                                                                                                                                  AATGAAGACTGGTGTGTCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                                                                                                                                                                                                                                                                                                               6730 BP; 2123 A; 1184 C; 1206 G;
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                           3.1%;
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                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                Score 47.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                    ed. No. 1.8;
Mismatches
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                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                 2217 T;
                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide for with cell signaling
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Best Local S
Matches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventior useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the monoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL06755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 14747; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 14747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                      GTGGCCAGTGGCTGTGCCACAGCTGTCGCATGAGCAAGCTCTCCCAGCCGCCCGGCCTCCT
                                                                                                                              graceanceregacerecraceaecraceaecaaecaaecaecaecaecaececeee
                                                                                                                                                                                                                                                                       AGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCT 585
  CATCCAAGGCCAGTTCCGTGGAGC
                                          CAGAGGAGCCCCGGCCCCAGGAGC
                                                                                                                                                                               GCCCCTCCAGCTTCCACCTGCAATGCCATGATCCACCGTTGAGCGAGGAGGACATACCCA
                                                                                                                                                                                                           GCCCTCGGGCCTTCCACCTGGCCTGCCTGCCCTCCGCTCCGGGAG-----ATCCCCA
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ilarity 55.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  793 A; 935 C; 890 G; 605 T; 0 U; 0 Other;
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Pred. No. 1.8;
0; Mismatches
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RESULT 91
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AAV24559
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Matches
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                               This sequence encodes the leukocyte specific protein, Sp140 of the invention. The Sp140 polypeptides act as gene transcription regulators. They can be used to develop products for use in the diagnosis and treatment of autoimmune diseases such as primary biliary cirrhosis, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, scleroderma and multiple sclerosis, viral diseases including those caused by herpes simplex virus, cytomegalovirus, HTV, hepatitis virus, human T-cell leukaemia, particularly acute promyelocytic leukaemia, cancers of the breast, ovary, prostate, bone, liver, pancreas or spleen, sarcomas and
                                                                                                                                                                                                         Sequence 2905 BP; 874 A; 610 C; 760 G; 661 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 54-57; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated gene transcription regulator, Sp140 - used to develop products for the diagnosis and treatment of auto-immune diseases, viral infections or cancers.
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P-PSDB; AAW57747.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sp140; leukocyte specific autoimmune disease; viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9814569-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BLOC/) BLOCH D B.
                                                                                                                                                                       Local
                                                    1876
                                                                                                       1816
                                                                                                                                                                       Similarity
                                                                                                                    CCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTG
                                                    TTĠCĠĂĊACTTĠTTĊAAĠAĠTĊŢŢĊĊAŢĠAĠĠAĊŢĠŢĊACAŢĊĊĠĠĊĊ
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                                                                                                      CCCTTGTATGAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US017715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/product="Sp140"
                                                                                                                                                                 3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; gene transcription regulator; therapy;
infection; cancer; ds.
                                                                                                                                                        Score 47.2; DE Pred. No. 2.1; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding sequence
                                                                                                                                                                                   DB
                                                                                                                                                         38;
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                                                                                                                                                                                Length 2905;
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                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conditions of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal converted in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colling and polynucleotide sequences have applications in colling sequences. Assets, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and conditions are did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                  Best Loc
Matches
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                                                                                                                                                              Sequence 2911 BP; 878 A; 609 C; 759 G; 665 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 11248; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73
                                                                                                                  Similarity
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                                                           CCTGTGCCAGAAGATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTG
 crereacecrecereeecrrecacereecreecreeccree 622
                                   CCCTTGTATGAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTG
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ilarity 64.8%;
Conservative (
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2000US-00649167
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                                                                                                Score 47.2; DB Pred. No. 2.1; 0; Mismatches
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                                                                                                                              Length 2911;
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1876 TTGCGACACTTGTTCAAGAGTCTTCCATGAGGACTGTCACATCCCGCC 1923

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                                                                                                                                                                                                                                                                       sequences: (I) is useful as hybridisation probes, polymerase chain (reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed concerning of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The CC diagnostice, forensics, gene mapping, identification of mutations (CC diagnostics, forensics, gene mapping, identification of mutations (CC diagnostics, forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the printed specification.
                                                                                                                                               Query Match
Best Local S
Matches 70
                                                                                                                                                                                                                          Sequence 3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated
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                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                     2168 CCTTGTATGAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGGAGGGGAGGTTTCTG
 2228 TIGCGACACTIGITCAAGAGICTICCATGAGGACTGICACATCCCGCC
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                                                                                                                                                                    Similarity
                             CCTGTGCCAGAAGAATGAGGACGAGTGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTG
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                             Score 47.2; DE Pred. No. 2.1; 0; Mismatches
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584 CTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCC-----GCTCCGGGAGATCC

647 636

GAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGGAGGGGAGCTGTTCTGTTGCGACAC

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RESULT 93
AAS75445
ID AAS75475
XX AAS75
XX AAS75
XX DNA e
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                                                                        Query Match
Best Local Similarity
Matches 106; Conserv
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                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                  Sequence 1210 BP; 248 A; 321 C; 368 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG11258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
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food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #11249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC.
       GAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGG 583
                                                                            Conservative
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57.9%;
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                                                                                                                Score 47;
Pred. No.
                                                                                Mismatches
                                                                                                                                                                                                                      273 T; 0 U; 0 Other
                                                                                                                                                 DB 5;
                                                                            70;
                                                                                                                                                 Length 1210
                                                                                Indels
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                                                                            7;
                                                                                Gaps
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SULT 94 S29014 star AAS29014; 21-NOV-2001 Genomic seque Human; uterir menstrual cyc Homo sapiens W0200155201-7 02-AUG-2000 04-FEB-2000 04-FEB-2000 01-MAR-2000 01-JUL-2000 01-JUL-2000 01-JUL-2000 01-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000	Db 648 TTGTTCAAGAGTCTTCCATGAGGACTGTCACATCCCGCCTGTGGAAGCTGAGAGGGATCT 707 Oy 637 CCAGTGGGACCTGGAGGTGCCAGCCTGCCAGCAACAGTCCAGGAGGTGCAGCCCC 696
08-SEP 2000 2000US 08-SEP 2000 2000US 14-SEP 2000 2000US 25-SEP 2000 2000US 25-SEP 2000 2000US 26-SEP 2000 2000US 27-SEP 2000 2000US 29-SEP 2000 2000US 29-OCT 2000 2000US 20-OCT	05-SER-2000; 2000US-0229509 05-SER-2000; 2000US-0229513 06-SER-2000; 2000US-0230437 06-SER-2000; 2000US-02310438 08-SER-2000; 2000US-0231243 08-SER-2000; 2000US-0231243 08-SER-2000; 2000US-0231243

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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Best Local Similarity
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11-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
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11-DEC-2000
11-DEC-2000
11-DEC-2000
11-DEC-2000
11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel human uterine motility-association polypeptides (AAU18094-AAU1812), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS28995-AAS29020 represent genomic sequences encoding for novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                              Sequence 6610 BP; 1208 A; 2130 C; 2123 G; 1149 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                                                           GCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCCGCTGCCTTCC
                         ATGACCTGGAGTCCCTTCTGAGCGAGC 1212
                                                                           GCCTGGCCCTGGGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGG
                                                                                                                                        CCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCAGCCCCGCCC
                                                                                                                                                                                                                             GCTGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCGCGATCGCTACTGCCAGTGCTTCC
GTGAGGCGGGTCCCAGCCTTCCCTAGC
                                                      ACTG-TCGCGAGCCGTGCCCCGGCCGGCTTCTACGGCTTGGGCTGTCGCCG---CCGGTAA
                                                                                                                                                                        GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
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2000US-02492119

2000US-02492149

2000US-02492449

2000US-02492659

2000US-02492659

2000US-02492699

2000US-02492999

2000US-02492999

2000US-02492999

2000US-02593919

2000US-02519309

2000US-02519399

2000US-02518689

2000US-02518699

2000US-02519909

2000US-02519909

2000US-02519909

2000US-02518699

2000US-02519909
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                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                     3.0%;
53.6%;
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Pred. No.
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14-AUG-2000
12-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
24-AUG-2000
25-SEP-2000
01-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence #19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 menstrual cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; uterine motility-association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
2000US-0190076P

2000US-019123P

2000US-020551EP

2000US-021513SP

2000US-021647P

2000US-021647P

2000US-02114886P

2000US-0217486P

2000US-0217487P

2000US-022964P

2000US-022513P

2000US-0225214P

2000US-0225214P

2000US-0225214P

2000US-0225214P

2000US-0225214P

2000US-0225214P

2000US-0225268P

2000US-0225758P

2000US-0231244P

2000US-0231244P

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2000US-0231244P
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2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
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RESULT 96
AAS26967
ID AAS26
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AC AAS26
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DT 07-NC
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel human uterine motility-association polypeptides (AAU18094-AAU18152), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS28995-AAS29020 represent genomic sequences encoding for novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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01-DEC-2000

05-DEC-2000

05-DEC-2000

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06-DEC-2000

08-DEC-2000

08-DEC-2000
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               07-NOV-2001
                                            AAS26967;
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                                                                                                                                                                                                                                                                                    CCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCCAGCCCCGCCC
                                                                                                                                                                                                                                                                                                                                            GCGGGGTGTGCGAGAGATGGTACGGACGTGCTGCGTTACTCACTGCCCCGCTGCCTTCC
                                                                        standard;
                                                                                                                                                                           ATGACCTGGAGTCCCTTCTGAGCGAGC 1212
                                                                                                                                                                                                     GCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGG 1185
                                                                                                                                               GTGAGGCGGGTCCCAGCCTTCCCTAGC
                                                                                                                                                                                                                                                                                                                           GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
                                                                                                                                                                                                                                                                 ACTG-TCGCGAGCCGTGCCCCGCCGGCTTCTACGGCTTGGGCTGTCGCCG----CCGGTAA
                                                                                                                                                                                                                                                                                                                                                                                     GCTGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCC
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2000US-0250391P
2000US-0251330P
2000US-0251988P
2000US-0251479P
2000US-0251866P
2000US-0251869P
2000US-0251869P
2000US-0251869P
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2000US-0251869P
2000US-0251869P
2000US-0251869P
2000US-0251969P
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             (first entry)
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Pred. No. 2.6;
0; Mismatches
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2000US-023196P 2000US-023196P 2000US-023239P 2000US-023239P 2000US-0233063P 2000US-0233063P 2000US-0234274P 2000US-0234274P 2000US-0234274P 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-023632P 2000US-023632P 2000US-023633P 2000US-023633P 2000US-023633P 2000US-023633P 2000US-02467P 2000US-02467P 2000US-0241809P 2000US-02467P 2000US-024921P 2000US-024929P 2000US-024929P 2000US-024929P 2000US-024929P 2000US-024929P 2000US-024929P

14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-OCT-2000
02-OCT-2000
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02-OCT-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
03-NOV-2000
03-NOV-2000
04-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
01-NOV-2000

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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC in diagnosing a pathological condition or susceptibility to a condition. Antibodies to the proteins can also be used in CC alleviating symptoms associated with the disorders and in diagnostic CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CC nervous system disorders e.g. hlzheimer's disease, infections caused by acteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before CC respensate tissues and in chemotaxis. The polypeptides can also be used to as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, cc and other nutritional components. The present content, lipid, protein, carbohydrate, vitamins, the invention. Note: The sequence data for this patent did not form part
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05-DEC-2000; 2000US-0251479P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
11-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0251990P.
05-UAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 303; 601pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 53.6
mes 143; Conservative
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                                                                                                                                                                                                                                                                                              CCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCAGCCCCAGCCCC
                                                                                                                                                                                                                                                                                                                                                                GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
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                                    GTGAGGCGGGTCCCAGCCTTCCCTAGC
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53.6%;
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Pred. No. 2.6;
0; Mismatches 120;
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ARS26968
ID ARS26
XX ARS26
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XX O7-NO
DE Human
XX Human
XX Human
XX Human
XX W Cardi
KW Cardi
KW W Cardi
KW Cardi
KW W Drese
CX W O2-NO
XX W D12he
XX W 17-JA
XX 17-J
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
26-JUL-2000
14-AUG-2000
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16-SEP-2000
01-SEP-2000
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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     2000US-019076P

2000US-0205515P

2000US-0205515P

2000US-02151356P

2000US-0215135P

2000US-021647P

2000US-0217486P

2000US-0217486P

2000US-022964P

2000US-0229513P

2000US-0225213P

2000US-0225214P

2000US-0225266P

2000US-0225266P

2000US-02252679P

2000US-0225275P

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2000US-0180628P
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2000US-0189874P
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Query Match Best Local S Matches 143

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Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; hizhelmer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; wound healing; epithelial cell proliferation; skin ageing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , a . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                               encoding partial novel secreted protein,
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12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0231242P. 2000US-0231243P. 2000US-0231243P. 2000US-0231413P. 2000US-0231413P. 2000US-0232080P. 2000US-0232081P.

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                                                                                                                                                                                                                                                                           The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a CC pathological condition. Antibodies to the proteins can also be used in CC alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoasorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac nervous system disorders e.g. cardiovascular disorders e.g. cardiac nervous system disorders e.g. cardiovascular disorders e.g. cardiac nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before CC regenerate tissues and in chemotaxis. The polypeptides can also be used to an another presentive to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, CC minerals, cofactors and other nutritional components. The present cC minerals, cofactors and cher nutritional components. The present of the invention. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                             Query Match
Best Local S
Matches 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476222/51.
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                  ACTGGCGCTGCCACTTCCCAGCCGGGACCTCCCGGGCCCGGGACGGCCTGCGCTGCAGAT
                                                                                                                                                                GCGGGGTGTGCCGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCCGCCTTCC
ACTG-TCGCGAGCCGTGCCCCGCCGGCTTCTACGGCTTGGGCCTGTCGCCG---CCCGGTAA
                                                                     GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
                                                                                                                                          GCTGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCC
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nilarity 53.6%;
Conservative
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2000US-0249265P

2000US-0249269P

2000US-0249299P

2000US-0249399P

2000US-025939P

2000US-025939P

2000US-0251339P

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2000US-0251866P

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                                                                                                                                                                                                           ; Score 47; DB 4; Pred. No. 2.6; 0; Mismatches
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2000US-023196PP
2000US-023239PP
2000US-023239PP
2000US-02332401PP
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2000US-0233063PP
2000US-0234274PP
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2000US-0235836PP
2000US-023637PP
2000US-023637PP
2000US-023637PP
2000US-023637PP
2000US-023637PP
2000US-023637PP
2000US-024687PP
2000US-024887PP
2

002 (first entry) 002 (first entry) 003 (first entry) 004 SEQ ID NO: ene therapy; neural disorder; reproducti y disorder; reproducti y disorder; cardiovas ative disorder; 1150 001. 2000US-0180628 000; 2000US-0180628 000; 2000US-0180350 000; 2000US-0180350 000; 2000US-0205515P 000; 2000US-0205515P 000; 2000US-0215135P 000; 2000US-022511P 000; 2000US-022511P 000; 2000US-022511P 000; 2000US-0225179P 000; 2000US-022579P 000; 2000US-022579P 000; 2000US-0225718P	Oy 1126 GCCTGGCCCTTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCGGCTCTGCACAGGG 1185
PR 14-SEP-200 PR 14-SEP-200 PR 14-SEP-200 PR 14-SEP-200 PR 14-SEP-200 PR 14-SEP-200 PR 21-SEP-200 PR 21-SEP-200 PR 21-SEP-200 PR 21-SEP-200 PR 22-SEP-200 PR	05-SEP- 05-SEP- 06-SEP- 06-SEP- 08-SEP- 08-SEP- 08-SEP- 08-SEP- 08-SEP- 08-SEP- 08-SEP- 12-SEP- 11-SEP-
000 2000US -0232399P. 000 2000US -0232399P. 000 2000US -0232401P. 000 2000US -0233063P. 000 2000US -0233063P. 000 2000US -0233063P. 000 2000US -0233934P. 000 2000US -023499P. 000 2000US -0235934P. 000 2000US -0235937P. 000 2000US -0235937P. 000 2000US -0235939P. 000 2000US -0236369P. 000 2000US -0236369P. 000 2000US -0236999. 000 2000US -0236999. 000 2000US -0236999. 000 2000US -0241787P. 000 2000US -0241789P. 000 2000US -024178P. 000 2000US -024178P. 000 2000US -0244617P. 000 2000US -0244617P. 000 2000US -0244617P. 000 2000US -024661P. 000 2000	0; 2000US-022950 0; 2000US-022951 0; 2000US-023043 0; 2000US-023043 0; 2000US-023122 0; 2000US-023122 0; 2000US-023144 0; 2000US-023144 0; 2000US-02320 0; 2000US-02320 0; 2000US-02320 0; 2000US-02320 0; 2000US-02320 0; 2000US-02320

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01-DEC-2000;
01-DEC-2000;
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
09-DEC-2000;
                                                                                                                                                                                                                                                                                         Sequence 6610
                                                                                                                                                                                                                                                                                                         The present invention provides human cDNAs, proteins and related gen DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequis a genomic DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                     polypeptide condition.
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                        Isolated
                                                                                                                  1126
                                                                                                                                                                                            1006
                                                           243
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                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid molecule encoding an inflammation-associated ide is used in preventing, treating or ameliorating a medical
                                                                            ATGACCTGGAGTCCCTTCTGAGCGAGC 1212
                                                                                                                 GCCTGGCCCTGGGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGG
                                                                                                                                                 CCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCAGCCCCAGCCCC
                                                                                                                                                                          GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
                                                                                                                                                                                      ACTGGCGCTGCCACTTCCCAGCCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGAT
                                                                                                                                                                                                             GCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCC
                                                                                               Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0249216P
2000US-0249218P
2000US-0249218P
2000US-0249244P
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ilarity 53.6%;
Conservative
                                                                                                                                    -TCGCGAGCCGTGCCCCGCCGGCTTCTACGGCTTGGGCTGTCGCCG---CCGGTAA
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                                                                                                                                                                                                                                                 Score 47; DB 4; Length 6610; Pred. No. 2.6; 0; Mismatches 120; Indels
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10-JAN-2002 genomic (first entry) DNA ID NO: 924.

Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal di pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation; ds. disorder;

02-AUG-2001 WO200154474-A2

17-JAN-2001; 2001WO-US001349

31-JAN-2000 04-FEB-2000 24-FEB-2000 02-MAR-2000 16-MAR-2000 17-MAR-2000 18-APR-2000 19-MAY-2000 07-JUN-2000 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 2000US-0179065P.
2000US-0184664P.
2000US-0184664P.
2000US-0194664P.
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11-JUL-2000
26-JUL-2000
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15-AUG-2000
16-SEP-2000
01-SEP-2000

ABA06838

standard;

DNA;

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RESULT 100
ABT07848
ID ABT078
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AC ABT078
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DT 14-NOV
DT 14-NOV
E
DE Novel
XX
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KW IMMUNO
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11-DBC-2000;
Immunostimulant; antirheumatic; antiarthritic; neuroprotective; antiallergic; antidiabetic; antiastimatic; antialfammatory; nootropic; immunosuppressive; anticoagulant; thrombolytic; antiatherseclerotic; cytostatic; nephrotropic; antiparkinsonian; gynecological; virucide; antibacterial; antiarrhythmic; fungicide; HFNAFO5; HFNABAS5; HFNBMO1; immunodeficiency; autoimmune disorder; allergic reaction; cardiovascularinflammatory condition; graft-versus-host disease; reproductive system; blood-related disorder; hyperproliferative; endocrine; neurological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides human cDNAs, proteins and related gen DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequences and inflammation of the present sequences are supported to the present sequences.
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14-AUG-2000;
Novel polypeptide useful for diagnosis, prognosis, prevention, treatment of immune, hyperproliferative, renal, respiratory,
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(RUBE/)
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Best Local Similarity
Matches 143; Conserv
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US-08-92-686-1
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Patent NO. 6329517
GENERAL INFORMATION:
APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITILE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUT
FILLE REFERENCE: 8484-0030-999
CURRENT APPLICATION NUMBER: US/08/913,832A
CURRENT FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: PCT/DE96/00444
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(5736)
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; LOCATION: (1)...(5736)
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GENERAL INFORMATION:
APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0043-999
FILE REFERENCE: 115/09/158,707
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SOFTWARE: FastSEQ for
SEQ ID NO 1
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APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERWATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0059-999
CURRENT APPLICATION NUMBER: US/09/249,181A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/913,832
PRIOR APPLICATION NUMBER: US 08/913,832
PRIOR APPLICATION NUMBER: US 08/913,832
PRIOR APPLICATION NUMBER: PCT/DE96/00444
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 1996-03-08
NUMBER OF SEQ ID NOS: 1996-03-08
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                                                                                 Matches
                                                                                                                                                                                                                        LENGTH: 6328
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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CURRENT FILING DATE: 1998-09-22
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LOCATION: (1)...(5736)
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1109 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGATACCTGTCCCC 1168
                         532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACCGCTGCCCTC 591
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                                                                                                  Similarity
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                                                                             3.9%;
ilarity 61.5%;
Conservative
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Pred. No. 3.2e-05;
0; Mismatches 60
                                                                             Score 60; DB 4; Le
Pred. No. 3.2e-05;
0; Mismatches 60;
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                                                                                 Indels
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 325
FERGTH: 6475
FIRES DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
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                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (219)..(5957)
US-09-620-312D-325
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/52,317
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR PILING DATE: 2000-01-21
NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
APPLICANT: Tang, Y
APPLICANT: Liu, C
APPLICANT: Asundi
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                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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1447
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                                                                                                            592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                    532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
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GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1482
                                 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                           GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA 1228
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Zhou, Ping
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Yang, Yonghong
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                           3.9%;
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                                                                                                                                                                                                                           Score 60; DB 4;
Pred. No. 3.3e-05;
0; Mismatches 60
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                                                                           1446
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RESULT 5 US-07-945-295-1

Sequence 1, Application US/07945295 Patent No. 6610823 GENERAL INFORMATION:

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RESULT 6
PCT-US91-06418-2
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                                                                                                                            Sequence 2, Application PC/TUS9106418 GENERAL INFORMATION:
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Best Local Similarity
Matches 103; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 1053 base pair
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 100 Peachtree Street
                                                                     APPLICANT: Oklahoma Medical Research, Foundation, TITLE OF INVENTION: Antigens Associated with PolynTITLE OF INVENTION: and with Dermatomyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: Human thymocyte lambda
CLONE: L1
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REFERENCE/DOCKET NUMBER: OMI
TELECOMMUNICATION INFORMATION:
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APPLICANT: Ge, Qun
TITLE OF INVENTION:
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE:
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CURRENT APPLICATION DATA:
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CITY: Atlanta
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                                                                                                                                                                                                                                            368
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Pred. No. 2e-05;
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                                                                                          Polymyositis
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PCT-US91-06418-2
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                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                   Sequence 1, Applic
Patent No. 6183988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 103;
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Best Local Similarity 58.9%;
                                                                                                                                                                                                      GENERAL
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ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
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INFORMATION FOR SEQ ID NO:
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IMMEDIATE SOURCE:
                                                                                                                        INERAL INFORMATION:
APPLICANT: Bloch, Donald B.
APPLICANT: Bloch, Kenneth D.
TITLE OF INVENTION: LEUKOCYTE-SPECIFIC PROTEIN
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/579023
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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                                                  STREET:
                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1053 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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             WASHINGTON D.C.
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                                                                                                                                                                                                                                                                                                                                    GCTGCCCTCACTGTGAGAAGGAGGGGGGGTCCAGTGGGAGGCCCAAGGAGGAAGAAGA 422
                                                                                                                                                                                                                                                                                                                                                                     GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
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f: US
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                                                  E: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C. 1100 NEW YORK AVENUE, N.W. SUITE 600
USA
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Pred. No. 2e-05;
0; Mismatches 72;
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                                                                                ; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: misc_feature
; OTHER INFORWATION: Incyte ID No.
US-09-976-594-1064
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                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                  SOFTWARE: PERL Program
SEQ ID NO 1064
LENGTH: 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 70; Conserv
  Query Match 2.9%;
Best Local Similarity 50.7%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1064, Application US/09976594 Patent No. 6673549
                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-10-12 PRIOR APPLICATION NUMBER: 60/240,409 PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-3/1-11
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1143
                                                                                                                                                                                     TYPE: DNA
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CLASSIFICATION: 51",
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,347
APPLICATION NUMBER: 02-0CT-1996
514
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NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.4330001/JAG/BJD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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  Score 44.6; DB 4; Length 2327; Pred. No. 0.15; 0; Mismatches 104; Indels 0
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US-08-340-203A-1
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                                                                                            Matches 107;
                                                                                                     Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE
                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4616 base pairs
TYPE: nucleic acid
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NAME: Haile, ph.D., Lisa A.
REGISTRATION NUMBER: p-38,3
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                             CLONE: HIC-1 polynucleotide
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STATE: California
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4225 Executive Square, Suite 1400
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                                                                                       Score 44.6; DB 1;
Pred. No. 0.19;
0; Mismatches 104;
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US-08-452-567-1/c
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US-08-452-567-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/039003 (Div PD3664)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4616 ---
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
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                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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STATE: California
                                                                                                                                                                                                                                                                                                 NAME/KEY:
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2091
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                                                              2151 GCCAGGCCGAGCGGGGCCCCCCGGGCGAGACGGCCGCGTCCCCACCACGCTCTTCGCAG
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                             688 TGCAGCCCCGGCAGAGGAGCCCCCGGCCCCAGGAGCCCACCCGTGGAGACCCCCGCTCCCCC
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                                                                                                                                                                                             Score 44.6; DB 2; Length 4616; Pred. No. 0.19; 0; Mismatches 104; Indels 0
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RESULT 11
US-08-452-427-1/c
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US-08-452-427-1
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Best Local Similarity 50.7
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: """
STREET: LA Jolla
CITY: LA Jolla
CTATE: California
""A
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CORRESPONDENCE ADDRESS
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APPLICATION NUMBER: US
FILING DATE: 15-NOV-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baylin, Stephen B. APPLICANT: Wales, Michele M.
                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: HIC-1 polynucleotide
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CGGGGCTTAGGTCGGCGGGAGAGGAGGTAAG
                                                        CGCTCGCTGGGGGAGCCGCCCTCCCGGCCCAGCTCGTCGCCATAGCTACCCAGGCCCGGC
                                                                                          TGCAGCCCCGGCCAGAGGAGCCCCCGGCCCCAGGAGCCCACCCGTGGAGACCCCGCTCCCCC 747
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US-09-085-407-1/c
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Best Local Similarity
Matches 107; Conserv
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APPLICATION NUMBER: US/08/340,20

FILING DATE: 15-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: 0-38,347

REFERRANCE/DOCKET NUMBER: 07265/

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
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APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE,
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
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STREET: 422
CITY: La Jolla
CTATE: California
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IMMEDIATE SOURCE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4616 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                  CLONE: HIC-1 polynucleotide
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2031 TCGTGCTTCATCCAGCGATAGAGGAGACTAG 2001
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                                                                                                                            CGGGGCTTAGGTCGGCGGGAGAGGAGGTAAG
                                                              CGCTCGCTGGGGGAGCCGCGCTCCCGGCCCAGCTCGTCGCCATAGCTACCCAGGCCCGGC
                                                                                            TGCAGCCCCGGCAGAGGAGCCCCCGGCCCCAGGAGCCCACCCGTGGAGACCCCCGCTCCCCC
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                                                                                                                                                                                                                                                                       Score 44.6; DB Pred. No. 0.19;
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US-09-920-923B-36
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Query Match
Best Local Similarity 50...
105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09526400
Patent No. 6566489
GENERAL INFORMATION:
APPLICANT: Goetinck, Paul F.
APPLICANT: Baciu, Peter C.
TITLE OF INVENTION: SYNDESMOS AND USES THEREOF
FILE REFERENCE: 10287-047001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEO ID NOS: 66
SOFTWARE: Patentin version 3.1
SEO ID NO 36
LENGTH: 882
                                                                                                                                          SEQ ID NO 3
LENGTH: 960
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Best Local Similarity
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/526,400 CURRENT FILING DATE: 2000-03-15 PRIOR APPLICATION NUMBER: 60/124,497 PRIOR FILING DATE: 1999-03-15 NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Unknown
                                                                                                         ORGANISM: Gallus
                                                                                                                           TYPE: DNA
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                  Score 42.6; DB 4;
Pred. No. 0.34;
0; Mismatches 104;
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RESULT 16
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US-09-526-400-1
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APPLICANT: Baciu, Peter C.
TITLE OF INVENTION: SYNDESMOS AND USES THERE
FILE REFERENCE: 10287-047001
CURRENT APPLICATION NUMBER: US/09/526,400
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,497
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 7
                                                                                               Sequence 1, Application PC/TUS9208258
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC. and ST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 105;
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Best Local Similarity
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LOCATION: (33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
             TITLE OF INVENTION: PRODUCTION OF CHUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1182
 ADDRESSEE:
STREET: 46
CITY: Sout
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ilarity 50.2%;
Conservative
 San Francisco
                                                                               H, INC. and PRODUCTION
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Pred. No. 0.37;
0; Mismatches 104;
                                                                               STATE OF OREGON BY AND OF GPA NEUROTROPHIC FA
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                                                                                   FACTOR
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Best Local Similarity
Matches 123; Conserv
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13712
                                                               Sequence 13712, Application US/09270767

Sequence 13712, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 13712

LENGTH: 3096
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225)3562
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MEDIUM TYPE: 5.25 inch, 360 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: single
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TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Johnston, Sean REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1040 GCCCGGGACGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGACCCCAGATGGCCG 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCCCGTCCGGCGGCCCCCCTTCCCCCTC 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGACAACCTGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCCTGGACATCTACGTGGAGCGGCAGGGCCTGGACGCCTCCATCAGCGTGGCGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTGGGACGGCCTGGGCCATGGCGGCGGCAGACACCCCTTCAGCCACCCTCCGGCA
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Pred. No. 0.4;
0; Mismatches 134;
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTMARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 4403765
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US-09-103-840A-2
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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      GGCCCTGCACCCCCTACTGTGTGGGGTCCT 911
                                           CGCCCGCCGTTGCCGCCGACACCGCCGCTGCCACCCCATACCGCCGGTACCGCCGACACCC 2956748
                                                                                                                             ACCGGTGCCGCCGACACCGCCGCCACCCACCAAGCCCGATGAGCGACCCAGC
                                                                                                                                                                                                             GGTGGTACCCGCGCCGCCGGCCACCGTTGCCGCCGCCACCACCGATGCCGCCGATGCC
                                                                                                                                                                                                                                                      AGAGGAGCCCCGGCCCCAGGAGCCCACCGGTGGAGACCCCGGCTCCCCCGGGGGCTTAGGTC
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ilarity 61.3%;
Conservative
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Pred. No. 7.2;
0; Mismatches 243;
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Pred. No. 7
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Sequence 60, Application US/09387286
Patent No. 6544733
GENERAL INFORMATION:
APPLICANT: Rommens, Caius M T
APPLICANT: Shang, Bei
APPLICANT: Shang, Bei
APPLICANT: Yan, Hua
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                                                                                                                                                RESULT 20
US-09-387-286-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
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Local Similarity 45.0%;
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Pred. No. 7.2;
0; Mismatches 243;
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FILE REFERENCE: r gene patent
CURRENT APPLICATION NUMBER: US/09/387,286
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: 60/098,402
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID 060
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GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1941 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3612
TYPE: DNA
ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RUBGER, DAVID C
APPLICANT: KUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: '
CORRESPONDENCE ADDRESS: '
THIBEAUL'
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND
REGISTRATION NUMBER: 27,83
REFERENCE/DOCKET NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OPPERMANN, HERMANN APPLICANT: OZKAYNAK, ENGIN
                                            ORIGINAL SOURCE:
                                                             MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: 617/248-7000
ORGANISM: no.
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 199110 CLASSIFICATION:
                                                                                                           STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                TYPE: NUCLEIC ACID
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Pred. No. 0.76;
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Patent No. 5670367
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Best Local Similarity
Matches 95; Conserv
                                                                                                APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPTELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)883-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1800 Diagonal Road, CITY: Alexandria
STRANDEDNESS:
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507..1703
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51.6%;
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/product= "HOP2"
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RESULT 23
US-09-312-762A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,898
FILING DATE: 20 FEB 1998
ATTORNEY/AGENT INFORWATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 916/10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MIA HOROWITZ ET AL.
TITLE OF INVENTION: EH DOMAIN CONTAINING GENES AND PROTEINS NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: an ASCI file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,762A
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                FILING DATE:
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1186
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                                                                                                                                                                                                                                                                                                                                                                                                                            2001 Jefferson Davis
                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 209; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                        Mark M. Friedman c/o Anthony Castorina
01 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%; Score 41.4;
3.1%; Pred. No. 1.
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RESULT 25
US-09-621-976-17202
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LENGTH: 4411529
TYPE: DNA
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Best Local Similarity 51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
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STRANDEDNESS: double
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Pred. No. 1.9;
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Pred. No. 14;
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138 SGGSCYKKKKKGKKGSCCMRSYMMCCYYYKRARRMMWKGGSCMMYTKRMMRRMCCCCMRR 197

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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TILE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17202
LENGTH: 364
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17202
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US-09-621-976-16656
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                                                                                                                                                                   SOFTWARE: Patent.pm
SEQ ID NO 16656
LENGTH: 430
TYPE: DNA
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APPLICANT: Dumas Milne Edwards, J.B.
                                                         Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 56;
                                                                                                                                   ORGANISM: Homo sapiens
-09-621-976-16656
                                                                                                                                                                                                                                               APPLICANT: GIORDANO, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1142 TGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1022 CCCAGCCGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGT 1081
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               442 GGAGCTGTTTTGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASTRMSSASCMMYMMMSAGSYASCAWKMSKYRRCAKWSCTYSWYMRASMKKSKYCAWSR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGAGCGAGCACACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRYSKKGSRGRWYWKKGCSRATSKKGRMMWKKKGSRRRÅTSRYGMMSSMYGASKRMSSMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGSMGWSGCSCSKRSWSRCRCMKSMWSWMMYMRSMKYKRSTCASCKYKGGKMACMTCWST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGTG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGSKCCMYSRKGSKSCYCCWGGSCCCCGCCAGCAGCAGGCAGGTGCCAGGCTGGGGTGCT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAMYRYMASYGWCYSYMARYYTCYSKYRMWKYCYRKYRSRGMCCMWCAGSGMCY-SRSAG
Conservative 121; Mismatches 128;
                                                         Conservative
                                                                         2.6%;
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                                                       87; Mismatches
 ::
                                                                       Score 40.6; DB Pred. No. 0.82;
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                                                                                           DB 4;
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                                                         91;
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                                                                                           Length 430;
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                                                       0;
                                                       Gaps
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TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THE
FILE REFERENCE: 2653-40
CURRENT APPLICATION NUMBER: US/09/724,797
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: 60/111,325
PRIOR FILING DATE: 1998-12-07
NUMBER: OF SEQ ID NOS: 95
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
LENGTH: 3033
RESULT 28
US-08-881-857-1
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; LOCATION: (1)...(3033)
US-09-724-797-81
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Patent No. 6733998
GENERAL INFORMATION:
APPLICANT: Jon S. THORSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacteria FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                1777
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                                                                                                                                                                                                                                                                            GCAGATCCTGCTCAGGAGACGTGACCCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCCAGCC 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTG
                                                                                                                                                                                                      cceccceccreeccreeccreeccaaeareacacreccaercaceaeccecrerec 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCCCTGCACCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCMMMWKRARKKKYMMMAMSRMSKYMARRRGSMMCYYYKSM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSMRRRRMCMWKGSYTYCYKSSSMMCMARRWKRARGKKRMCCYTKGGGRMMRKYCCMRKK
                                                                                  CGAG 1714
                                                                                                                                                                                                                                                GCGCCTCCGGCTCGCGGGCCAGCAGGTCGGCGGCGTAGCGGGAGGAGGAGCACCCGGG
                                                                                                                                                                                                                                                                                                                              CCTCGCAGAGCACCCCGCTCGGCCGGGGGGGTCAACTCGCTCTCCTCCGGCCAGCATCCGCA 1838
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                                                                                                                                                                CCAGCCGGCCGGCCCGGAGTCGCGCAGCAGCCAGGTACCAGGGCGTGCTGC
                                                                                                                                                                                                                                                                                                                                                                  CCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCT 1059
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Pred. No. 1.8;
0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3033;
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Sequence 1, Application US/08881857 Patent No. 5919660

ENERAL INFORMATION:

APPLICANT:

KIKLY,

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                                                                                                                                                                                                                                                                                                                                   RESULT 29
                                                                       APPLICANT: KIKLY, KRISTINE K.
APPLICANT: GROSS, MITCHELL S.
APPLICANT: HURLE, MARK ROBERT
TITLE OF INVENTION: HUMAN REQUIEM
FILE REFERENCE: ATG-50013-1
CURRENT APPLICATION NUMBER: US/09/233,342A
CURRENT FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: 08/881,857
PRIOR APPLICATION NUMBER: 08/881,857
PRIOR APPLICATION NUMBER: 08/881,857
PRIOR FILING DATE: 1997-06-24
                                                                                                                                                                                                                                                      Sequence 1, Application US/09233342A Patent No. 6207803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-0
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Win
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/881,85
PILING DATE: 24-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,229
PILING DATE: 26-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 37G-500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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les 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1073
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                                                                                                                                                                                                                                                                                                                                                                                                                               19482
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                                      1996-06-26
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Windows Version 3.0
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                                                           60/021,299
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Pred. No. 1.6;
0; Mismatches 48; Indels 0
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US-09-620-312D-389/c
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Dunrui
APPLICANT: wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
TITLE OF INVENTION: No. 6569662el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: 2009/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
COMMUNER: 5 FET SEGS 1105
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LENGTH: 1556
                                                                                                                                                                                                                                                                                                                      SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.0
Best Local Similarity 59.0
Matches 69; Conservative
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                                                                                                                                     Matches 105;
                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang,
                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (25)..(1197)
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT
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                                                                                                                                                                                                                                                                                                         ENGTH: 1682
                                1024 CAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCAGATCCTGCTCAGGAGACGTGA 1083
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                                                                                                  614 GTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCA 670
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Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
                                                                 GCACGGAGCACTGGCCCGGCATTCGCCGCTCCGTCGCCGCCCAGGGCGCCTCCTCCTCCG 158
CCCCGGTCGCATCTCGCAGCAGCTCCGCTACACCCTGGGCGCCCGGCGGAGGCACCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Xue, Aldong J.
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                                                                                                                                   Conservative
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di, Vinod
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No. 6569662el Nucleic Acids
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59.0%;
                                                                                                                                                  2.6%;
                                                                                                                                  <u>,,</u>
                                                                                                                                  Score 40.2; DB 4;
Pred. No. 1.6;
0; Mismatches 108;
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Pred. No. 1.6;
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RESULT 32
US-09-338-125-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compactive COMPUTER: IBM Compactive COMPUTER: FastSEQ Version 2.0 SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION NUMBER: US/08/969,10 FILING DATE: 13-NOV-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 7934-TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090 TELEPHONE: 212-790-9090
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                                                                                                                                                                                                                                                                                                                                                                                 US-08-969-106-9
Sequence 9, Application US/09338125
Patent No. 6521412
GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application Patent No. 5986055
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               Matches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2399 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: 81
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION: CI
NUMBER OF SEQUENCES: :
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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Nandabalan,
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Pred. No. 1.8;
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; FEATURE:
; NAME/KBY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549516H1
US-09-313-294A-604
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                                                                                                               SOFTWARE: PE
SEQ ID NO 604
LENGTH: 293
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APPLICANT: Lalgudi
                                                                                                                                                                                                                                                                                                                                                  Sequence 604, Application US/09313294A Patent No. 6476212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                                     APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORWATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,87
                                                                             TYPE: DNA
ORGANISM: Zea mays
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELEPHONE: 212-/-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                          PERL Program
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                                                                                                                                                                                                                                                                                                                Lalgudi, Raghunath
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1155 Avenue of the Amer.
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PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 11986

LENGTH: 762

TYPE: PARTY NUMBER: US 60/094,190
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US-09-252-991A-11986
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US-09-252-991A-11956
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11986
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                                                                                                                              Sequence 11956, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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APPLICANT: Marc J.
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Best Local Similarity
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 1.4;
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Pred. No.
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APPLICANT: Reynolds, Paul R.
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5.5
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; ORGANISM: Gallus gallus
US-08-680-506-5
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Best Local Similarity
Tatches 97; Conserva
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11956
LENGTH: 1125
TYPE: DNA
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GCATCCTGCAGTGGGCCATCCAGAGCATGGCCCGTCCGGCGGCGGCCCCTTCCCCTGAC 1284
                                                                                                                                                                                                                              GGACGGGCCTGCGGTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGG 1104
                                                                                                                                                                  TGCTGGCCCCAGCCCCGCCCGGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTC 1164
                                                                                                                                                                                                      GCGGCTACTTCGGCACCAAGTCCCGCTACGAGGAGGTGAACCCGCACCTGGCGGAGGACC
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Pred. No. 1.6;
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GENERAL INFORMATION:
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
FEARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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Patent No. 6008013
GENERAL INFORMATION:
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER APPLICATION NUMBER: 60/021,672
UMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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US-08-680-506-6
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US-08-680-506-8
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Best Local Similarity 44.9%;
Matches 150; Conservative
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                                                                                    SOFTWARE: PatentIn
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Mismatches 184; Indels
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; ORGANISM: Gallus
US-08-680-506-4
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SEQ ID NO 4
LENGTH: 2233
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Best Local Similarity
Matches 150; Conserv
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Best Local Similarity 44.9%;
Matches 150; Conservative
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CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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Pred. No. 2.5;
0; Mismatches 184;
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Pred. No. 2.2;
0; Mismatches 184;
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US-08-785-310A-4/c
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
I ENUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-70A1-1997
CLASSIFICATION: 536
ATTORNEY/ACENT
                                                                                                                                                                                                                                                                                                                  Query Match 2.6%;
Best Local Similarity 50.4%;
Matches 122; Conservative
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STRANDEDNESS: doub
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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CC 10
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                                                                GAGCCCACCGTCTGGCTGCAGCGGGTTGGCAGGACCCGAAGCCCAGGGCGGCTCGTG
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                                               SOFTWARE:
SEQ ID NO 1
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GENERAL INFORMATION:

APPLICANT: Reynolds, Paul R.

IITLE OF INVENTION: CHONDROCYTE PROTEINS

FILE REFERENCE: 176/60991

CURRENT APPLICATION NUMBER: US/08/680,506C

CURRENT FILING DATE: 1996-07-08

EARLIER APPLICATION NUMBER: 60/021,672

EARLIER FILING DATE: 1996-07-05

NUMBER OF SEQ ID NOS: 18
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LENGTH: 5027
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                                                                                                                      1285 CCCAGATGGCCGGGACATGCAGCTCTGATGAGAG 1318
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CGCTGGCCGCCTGGCCGATGTGGTACGAGGAGAG
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264

324

1104 144 1044

204

RESULT 42 US-09-679-279-1/c TITLE OF INVENTION: Recombinant Megalomicir TITLE OF INVENTION: Genes and Uses Thereof FILE REFERENCE: 300622004700 CURRENT APPLICATION NUMBER: US/09/679,279 CURRENT FILING DATE: 2000-10-04 PRIOR APPLICATION NUMBER: US 60/158,305 PRIOR APPLICATION NUMBER: US 60/190,024 PRIOR APPLICATION NUMBER: US 60/190,024 PRIOR APPLICATION NUMBER: US 60/190,024 PRIOR FILING DATE: 1909-10-08 GENERAL INFORMATION:
APPLICANT: McDaniel, Robert
APPLICANT: Volchegursky, Yan Sequence 1, Application US/09679279 Patent No. 6524841 NUMBER OF SEQ ID NOS: LENGTH: 47 ORGANISM: Micromonospora megalomicea 47981 FastSEQ for Windows Version 4.0 rsky, Yanina Recombinant Megalomicin Biosynthetic Rename and Uses Thereof

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NAME/KEY: misc_feature
LOCATION: (15427) ... (16476)
OTHER INFORMATION: megAI, ATI
NAME/KEY: misc_feature
LOCATION: (17155) ... (17694)
OTHER INFORMATION: megAI, KR1
NAME/KEY: misc_feature
LOCATION: (17947) ... (18207)
OTHER INFORMATION: megAI, ACP1
                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (12505)...(13470)
OTHER INFORMATION: megAI, AT-L
NAME/KEY: misc feature
LOCATION: (13576)...(13791)
OTHER INFORMATION: megAI, ACP-L
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OTHER INFORMATION: 7
OTHER INFORMATION: 8
NAME/KEY: CDS
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OTHER INFORMATION:
NAME/KEY: CDS
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (13849)...(15126)
OTHER INFORMATION: megAI, KS1
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OTHER INFORMATION: megBIV, TDP-hexose 4-ketoreductase,
OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 4-ketoreduct
OTHER INFORMATION: SEQ ID NO: 12= translated amino acid
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NAME/KEY: CDS
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OTHER INFORMATION: megAI; S
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OTHER INFORMATION:
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LOCATION: (5822)
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NAME/KEY: CDS
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INFORMATION: SEQ ID NO: 2=
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N: megDI, rhodosaminyl transferase (eryCIII homolog),
N: TDP-megosamine glycosyltransferase;
N: SEQ ID NO: 4= translated amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              megBV,
SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   megDIII,
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       megDII, deoxysugar transaminase (eryCI, DnrJ homolog).
TDP-3-keto-6-deoxyhexose 3-aminotransaminase;
SEQ ID NO: 6= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . (8206)
megDV, TDP-hexose 4-ketoreductase (eryBIV, dnmV homolog),
TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SEQ ID NO NO: 9= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             megDIV, TDP-4-keto-6-deoxyglucose 3,5-epimerase TDP-4-keto-6-deoxyhexose 3,5-epimerase; SEQ ID NO: 8= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          megG(megY),
SEQ ID NO: !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose
SEQ ID NO: 10= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mycarosyl transferase, mycarose glycosyltransferase, NO: 11= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I, daunosaminyl-N,N-dimethyltransferase
NO: 7= translated amino acid sequence
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5= translated amino acid sequence
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l sequence
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                                                         NAME/KEY: misc_feature
LOCATION: (42168)...(42425)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                          OTHER INFORMATION: megAIII, NAME/KEY: misc feature LOCATION: (39795)...(40811)
                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (38187)...(3
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: megAIII,
NAME/KEY: misc_feature
LOCATION: (37860)...(38120)
OTHER INFORMATION: megAIII,
                                                                                                                               LOCATION: (41406)...(41936)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                     OTHER INFORMATION: megAIII,
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                                        NAME/KEY:
                                                                                                                                                                                 NAME/KEY: misc feature
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                misc_fe: (42585)
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feature

ACP6

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AT6

(43271)

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) . . . (39470)

KS 6

ACP5

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OTHER INFORMATION: megAII, KS4
NAME/KEY: misc_feature
LOCATION: (28897)...(29931)
OTHER INFORMATION: megAII, AT4
NAME/KEY: misc_feature
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LOCATION: (24544)...(25581)
OTHER INFORMATION: megAII,
NAME/KEY: misc feature LOCATION: (37068)...(3)
                                     NAME/KEY: misc feature LOCATION: (35385)...(36419) OTHER INFORMATION: megAIII,
                                                                                         LOCATION: (33780)...(35027)
OTHER INFORMATION: megAIII,
                                                                                                                                                           LOCATION: (33666)...(43271)
OTHER INFORMATION: megAIII;
                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (33052)...(33312)
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (32257)...(3)
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (29953)...(30477)
OTHER INFORMATION: megAII, DH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (26230)...(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: megAI, NAME/KEY: misc_feature LOCATION: (22318)...(22575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: megAI, AT2 NAME/KEY: misc_feature
                                                                                                                      NAME/KEY: misc_fe
LOCATION: (33780)
                                                                                                                                                                                                                                                                              OTHER INFORMATION: megAII,
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: megAII, ER4
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LOCATION: (31396)...
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LOCATION: (29953)...(3
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LOCATION: (27393)...(28590)
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OTHER INFORMATION: megAII, ACP3
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OTHER INFORMATION: megAII, KR3 (inactive)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (22867)...(33555)
OTHER INFORMATION: megAII; SEQ ID NO: 14= translated amino acid sequence
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                                                                                                                                                                                                                      OTHER INFORMATION: megAII,
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  ... (37604)
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                                                                                                                                                                SEQ ID
                                             AT5
                                                                                                     KS5
                                                                                                                                                                NO: 15= translated amino
                                                                                                                                                                acid sequence
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Floppy disk

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US-08-998-416-723; Sequence 723, Application US/08998416; Patent No. 6239264
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Best Local Simi
Matches 155;
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OTHER INFORMATION: megBII-2(megBII), TDP-4-keto-6-deoxy-L-glucose
OTHER INFORMATION: TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
OTHER INFORMATION: SEQ ID NO: 18= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (46660)...(47403)
OTHER INFORMATION: megH, TEII; SEQ ID NO: 19= translated amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
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OTHER INFORMATION: SEQ ID NO: 17= translated amino acid sequence
                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                             APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES
TITLE OF INVENTION: AND USES THEREOF
COMPUTER READABLE FORM:
                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                  Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                           Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                           Mohr, Christine
                                     USA
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SEQ ID NO:
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Pred. No. 7.1;
0; Mismatches 169;
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RESULT 44
US-09-655-270A-2
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                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rouviere,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                             sequence 2, Application US/09655270A Patent No. 6329151
NUMBER OF SEQ ID NOS:
SOPTWARE: Microsoft
SEQ ID NO 2
LENGTH: 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.6%;
Best Local Similarity 46.3%;
Matches 130; Conservative
                                                                                                                                                 TITLE OF INVENTION: High Density Sampling FILE REPERENCE: BC1011 US NA CURRENT APPLICATION NUMBER: US/09/655,270A CURRENT FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 919-541-85
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30
TELECOMMUNICATION INFORMATION:
                                                                         PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
PRIOR APPLICATION NUMBER: 60/152,542
PRIOR FILING DATE: 1999-September-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 24-DEC-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                        1255 CCCGTCCGGCGCCCCCTTCCCCGACCCCAGATGGCC 1295
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Pred. No. 1.9;
0; Mismatches 151; Indels
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RESULT 46
US-09-955-597-2
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; ORGANISM: Rhodococcus erythropolis HL
US-09-651-941-2
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US-09-651-941-2
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US-09-655-270A-2
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                                                                                                                                             Sequence 2, Application US/09955597
Patent No. 6461856
GENERRAL INFORMATION:
APPLICANT: ROUVIER, PIERRE E
APPLICANT: WALTERS, DANA M
APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Acid
FILE REFERENCE: BC1022 US NA
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Best Local Similarity
Matches 92; Conserv
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SEQ ID NO 2
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APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Acid Degradation FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION NUMBER: US/09/651,941
CURRENT FILING DATE: 2000-08-31
PRIOR STPLICATION NUMBER: 60/152,545
DRIOR SEPLICATION NUMBER: 60/152,545
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CURRENT APPLICATION NUMBER: US/09/955,597
CURRENT FILLING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
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NUMBER OF SEQ ID NOS:
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Pred. No. 2.8;
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US-09-655-270A-1
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                                                                                                                                                                                                                  RESULT 48
                              Sequence 1, Application US/09651941 Patent No. 635470 GENERAL INFORMATION: APPLICANT: ROUVIER, PIERRE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 12508
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Best Local
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Best Local Similarity 51.1%;
Matches 92; Conservative
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TITLE OF INVENTION: High Density Sampling
FILE REFERENCE: BC1011 US NA
CURRENT APPLICATION NUMBER: US/09/655,270A
CURRENT FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
PRIOR APPLICATION NUMBER: 60/152,542
PRIOR FILING DATE: 1999-September-03
NUMBER OF SEQ ID NOS: 37
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Pred. No. 5.7;
0; Mismatches
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Pred. No. 2.8;
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APPLICANT:

APPLICANT: WALTERS, APPLICANT: RAINER, TITLE OF INVENTION:

RUSS Genes Encoding Picric Acid Degradation

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US-09-252-991A-12051/c
; Sequence 12051, Application US/09252991A
; Patent No. 6551795
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; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-1
                                                      RESULT 50
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CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 12523
TYPE: NAT
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 12523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09955597
Patent No. 6461856
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric
FILE REFERENCE: BC1022 US NA
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CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,545
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Rhodococcus erythropolis HL PM-1
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Pred. No. 5.7;
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Pred. No. 5.7;
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Sequence 11993, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO I
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILLING DATE: 1998-02-18

PRIOR FILLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 11993

LENGTH: 564
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LENGTH: 531
TYPE: DNA
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                   TYPE: DNA
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hes 96; Conserv
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11962
                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 14041
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                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13744
LENGTH: 708
TYPE: DNA
ORCANTO: -
                                                                                                                                 Sequence 13605, Appl Patent No. 6551795 GENERAL INFORMATION:
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APPLICANT: Marc J.
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                     1223
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                                                                                                                                                                        Application US/09252991A
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 2.7;
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Pred. No.
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PSEUDOMONAS

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APPLICANT: MARC J. Rubenfield et al.
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEU
FILE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13494
LENGTH: 984
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13494
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; PRIOR APPLICATION NUMBER: US 60
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEO ID NOS: 33142
; SEO ID NO 13605
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginos
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US-09-252-991A-13494
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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 118; Conserv
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Best Local Similarity
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TCCAAAGGCGGCGAACCTGCCGGCTGTCGATCAGGTGCTGGCTTTCGAGCAGGCCCTCGG
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47.2%;
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Pred. No. 3;
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Pred. No. 2.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4137
LENGTH: 1104
                                                                                                                                                              RESULT 58
US-09-252-991A-4071
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Sequence 4071, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Best Local Similarity
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TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS
FILE REFERENCE: 107196.136
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MATE J. Rubenfield et al.
VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
VENTION: THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4071
LENGTH: 1275
TYPE: DNA
CORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 59
US-09-894-998A-35/c
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                                                                                US-09-894-998A-35
                                                                                                                                                                                                                                                                           Sequence 35, Application US/09894998A
PATENT NO. 6537555
GENERAL INFORMATION:
APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
                                                                                                                                      PILE REFERENCE: 210121.538
CURRENT APPLICATION NUMBER: US/09/894,998A
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 2481
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Best Local Similarity 44.2%;
Matches 160; Conservative
  Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                               TYPE: DNA
ORGANISM: HSV-2
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ilarity 45.0%;
Conservative
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Pred. No. 3.3;
0; Mismatches 202;
  Score 38.8; DI
Pred. No. 4.1;
O; Mismatches
                                       DB 4;
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    177;
                                       Length 2481;
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RESULT 61
US-09-765-400-64
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LENGTH: 11958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wayne, Jay
APPLICANT: Wayne, Jay
APPLICANT: Xu, Shuang-Yong
TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
TITLE OF INVENTION: Wectors And Identification of Two Thermus Plasmid
TITLE OF INVENTION: Replication Origins
TILE REPERENCE: Thermus Shuttle Vector
CURRENT APPLICATION NUMBER: US/09/134,246B
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 30
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Local Similarity 50.3%;
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Pred. No. 7.9;
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Sequence 64, Application US/09765400 Patent No. 6691568 GENERAL INFORMATION:

APPLICANT: Ghazal,

Peter

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; APPLICANT: Huang, Huang; TITLE OF INVENTION: Generation of Human Cyto; TITLE OF INVENTION: Recombinants; FILE REFERENCE: 98,299; CURRENT APPLICATION NUMBER: US/09/765,400; CURRENT FILING DATE: 2000-11-03; NUMBER OF SEQ ID NOS: 64; SOPTWARE: Patentin version 3.1; SEQ ID NO 64; LENGTH: 229354
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                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 62
US-09-705-400-64
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                                                                                                                       US-09-705-400-64
                                                                                                                                                                                                       NUMBER: Patent:
SOFTWARE: Patent:
SEQ ID NO 64
'ENGTH: 229354
                                                                                                                                                                                                                                                      APPLICANT: Ghazal, Peter
APPLICANT: Huang, Huang
TITLE OF INVENTION: Generation of Human Cyt.
TITLE OF INVENTION: Recombinants
FILE REFERENCE: 98,299
CURRENT APPLICATION NUMBER: US/09/705,400
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 64
                                                          Query Match
Best Local S
Matches 124
                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/09705400 Patent No. 6692954
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 124; Conserv
                                                                                                                                                                        LENGTH: 229354
TYPE: DNA
ORGANISM: Human cytomegalovirus
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NAME/KBY: misc feature
OTHER INFORMATTON: Human cytomegalovirus strain AD169 (GenBank X17403.1)
                                                                                                                               PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human cytomegalovirus;
93012
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                 946 GCGGGGTTGCGGAGATGGTACCGGACGTGTCCTCACTGCGCCGCTGCCTTCC 1005
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GCGCAGTCCGCGGCAGGGTTCCGGCCGGTGCTGCGCACGCTGCGCCCCGCTCCCGCC
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49.8%;
                                                                       2.5%;
49.8%;
                                                       Score 38.6; DE
Pred. No. 21;
0; Mismatches
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                   Human Cytomegalovirus Yeast Artficial Chromosome
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                                                                                                                                     AD169 (GenBank X17403.1)
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                                                                                      Length 229354
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GENERAL INFORMATION:
APPLICANT: JON S. THORSON
TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GEN
TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESIST
FILE REFERENCE: 2653-40
CURRENT APPLICATION NUMBER: US/09/724,797
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/111,325
PRIOR TILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FASEUSEQ for Windows Version 4.0
ISBO ID NO 21
LENGTH: 1683
TYPE: DNA
OPCANITON. BOLOGIA
                                                                                                                                                                              RESULT 64
US-09-077-940A-3
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; NAME/KEY: CDS
; LOCATION: (1)...(1683)
US-09-724-797-21
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US-09-724-797-21
Sequence 3, Application US/09077940A
PATENT NO. 6576441
GENERAL INFORMATION:
APPLICANT: KIMURA, TOTU et al.
TITLE OF INVENTION: MOVEL SEMAPHORIN Z AND GENE
FILE REFERENCE: 0020-4426P
CURRENT APPLICATION NUMBER: US/09/077,940A
CURRENT FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09724797 Patent No. 6733998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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48.6%;
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Pred. No. 4.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                             770
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ENCODING

THE SAME

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RESULT 65
US-10-140-002-543
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Patent No. 6725730
                                                                                                                                                                                                                                                                                                                                         Patent No. 6725730 GENERAL INFORMATION:
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                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Best Local S
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               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
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LOCATION: (39)..(2
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: (2706)..(3524)
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NAME/KEY: 5'UTR
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
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Local Similarity 47.0%;
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                                                                                                                                                         Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCCACCCGTGGAGACCCCGCTCCCCC 747
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                                                                           Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                         DeForge, Laura
                                                                                                              Tumas, Daniel
                                                                                                                             Stewart, Timothy A.
                                                                                                                                              Smith, Victoria
                                                                                                                                                                                                                                                            Filvaroff, Ellen
                                                                                                                                                                                                                                                                          Desnoyers, Luc
                                                                                                                                                                                                                                                                                                         Beresini, Maureen
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NUMBER: US/10/140,002
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Pred. No. 5.8;
0; Mismatches 171;
                                              POLYPEPTIDES
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CURRENT FILING DATE: 2002-
Frior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 543
ENGTH: 3721
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-543
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US-09-191-171-7/c
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Best Local S
Matches 154
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Patent No. 6149909 6143294
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                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PEM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, W
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,171
FILING DATE:
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY SCOTT MURPHY
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/494,104
FILING DATE: 23-JUN-1995
                                                                                                                                                                                                                                                                                                                             APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPMOOD, JOHN J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE
TITLE OF INVENTION: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                            STATE: N
COUNTRY:
ZIP: 115
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nilarity 47.0%;
Conservative
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Pred. No. 5
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Mismatches
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RESULT 67
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Best Local (
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APPLICANT: SCOTT,
APPLICANT: ANSON,
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4480 base pairs
                                                                                                                                   APPLICANT: ORSBORN, Annette M. APPLICANT: NELSON, Paul V. APPLICANT: CLEMENTS, Peter R. APPLICANT: MORRIS, Charles P. APPLICANT: HOPWOOD, John J. TITLE OF INVENTION: SEQUENCES ENTITLE OF INV
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                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
STREET:
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STRANDEDNESS: single
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TELEFAX: 516-742-4366
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                                                   ADDRESSEE:
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                        E: SCULLY SCOTT MURPHY & PRESSER 400 Garden City Plaza
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Donald S.
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Pred. No. 6.3;
                                                                                                                                            ALPHA-L-IDURONIDASE AND ENCODING SAME
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US-09-639-696C-6/c
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                                                                                                                                                                    Sequence 6, Application US/09639696C Patent No. 6524835
GENERAL INFORMATION:
APPLICANT: SCOTT, Hamish S.
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US-09-385-707-7
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Best Local S
Matches 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8978
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 516-742-43
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/385,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
2320
                                                                                                                                                                                                                                                                                                                                        2558
                                                                                                                                                                                                                                                                                                                                                                                                                           2618
                                                                                                                                                                   2440 TCCCCAGGCCCGCCACGCGAGGCCGACCCCGGGAAGCGCGCGCGCTGGAGGAAGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150;
                                                                                                           ACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACC 891
CCCCAGCGGCCCCGGCTC 2303
                                                                                                                                                                                                                                                                                       GCCCCAGGAGCCACCCGTGGAGACCCCCGCTCCCCCGGGGCTTAGGTCGGCGGAGAGAG
                                                                                                                                                                                                                                                                                                                                        GCTGCTCCTCAT--CTGCGGGGGGGGGGGGGGGGCCGTCGCCGCGTGGGGTCGTTGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                           GGACGCCCACCGTGTGGTTGCTGTCCAGGACGGTCCCGGCCTGCGACACTTCGGCCCAGA
                                                                                                                                                                                                          AGGTAAGAGGTCCACCTGGGGAACCCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC 831
                                                                                                                                                                                                                                                      CGCCCCCGACCCAGGGCCGGGCCTCCCACCACTCGCTCCCCCTTCGCTGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                               GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCC
                                       CCCTACTGTGTGGGTC 909
                                                                                 Conservative
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Pred. No. 6.
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ORSBORN, Annette M.
NELSCON, Paul V.
CLEMENTS, Peter R.
MORRIS, Charles P.
HOPWOOD, John J.

SCOTT, Hamish ANSON, Donald

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2381

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2501 711 2559

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; MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: US-09-639-696C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                             4198
                                                                                                                                                                                                                                                      4258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6238 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            4316 GCTGCTCAT--CTGCGGGGGGGGGGGGGCCGTCGCCGCGTGGGGTCGTTGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      4376 GGACGCCCACCGTGTGGTTGCTGTCCAGGACGGTCCCGGCCTGCGACACTTCGGCCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON PEABODY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                  TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
                                                                                                                                                                                                                                                                                                     712
892 CCCTACTGTGTGGGTC 909
                                                                                                                                                                                                             772
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REGISTRATION NUMBER: 34,697
REFERENCE/DOCKET NUMBER: 2249/304
                                                                                                             Accrecceecroceccriceecaecceecreccaeercreeacrecreecceeccreeacc 891
                                                                                                                                                             TCCCCAGGCCCCGCCACGCGGAGGCCGACCCCGGGAAGCGCGCGCGCTGGAGGAAGTGCGC
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FILING DATE: 14-NOV-1991
APPLICATION NUMBER: AU PCT/AU92/00611
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/191,171
FILING DATE: 13-NOV-1998
APPLICATION NUMBER: US 08/494,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 990 Stewart Avenue CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 516-832-7572
TELEFAX: 516-832-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/639,696C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38.4;
Pred. No. 7.
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                                             US-09-252-991A-6641
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION UMBERS: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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SEQ ID NO 6674
LENGTH: 1260
                                                                                                             SEQ ID NO 6641
LENGTH: 2163
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6641, Application US/09252991A Patent No. 6551795
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Query Match
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR TILING DATE: 198-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                  ORGANISM: Pseudomonas
                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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                                                                aeruginosa
2.5%;
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Pred. No. 4.6;
0; Mismatches 138;
Score 38.2;
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  В
  4.
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  Length 2163;
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RESULT 71
US-08-289-112-1
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   Query Match 2.5%;
Best Local Similarity 51.5%;
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATIBLE PATENT RELEASE #1.0, VG SOFTWARE: PATENTIN PATA; PATENT APPLICATION DATA; APPLICATION NUMBER: US/08/289,112 FILING DATE: 10-APR-1994 CLASSIFICATION: 435 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Parker, David L. REGRERECES/DOCKET NUMBER: 32,165 REFERENCES/DOCKET NUMBER: UTSD:414/FTELECOMMUNICATION INFORMATION: TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Yanagi
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wh.
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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VENTION: Endothelin Converting Enzyme-1: A
VENTION: Membrane-Bound Metalloprotease That Cataly
VENTION: Proteolytic Activation of Big Endothelin-1
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APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFGI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08458568A Patent No. 5821339
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Best Local &
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/065,146
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
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APPLICATION NUMBER: US/08/458,568A
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STREET: One Liberty Place, 46th floor
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US-08-196-218-31
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                                         Sequence 31, Application US/08196218 Patent No. 5614619
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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NAME: GRUDER, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US91/065
FILING DATE: 1991/0910
CLASSIFICATION: 424
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               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                               Local 52;
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Illinois
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Piepersberg, Wolfgang
Stockmann, Michael
Taleghani, Kampiz Mansouri
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APPLICANT:

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                                                                                                                              RESULT 76
US-08-681-953-31
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US-08-196-218-31
Sequence 31, Application US/08681953
Patent NO. 5710032
GENERAL INFORMATION:
APPLICANT: Piepersberg, Wolfgang
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Grabley, S
APPLICANT: Sichel, Pe
APPLICANT: Brau, Barb
TITLE OF INVENTION: S
TITLE OF INVENTION: U
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME/KEY:
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NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,;
REFERENCE/DOCKET NUMBER:
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NAME/KEY:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Grabley, Susanne
Sichel, Petra
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Pred. No. 6.6;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
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NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/196,218
FILING DATE: 25-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US
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                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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2148
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1300 I Street, N.W.
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Grabley, Susanne
Sichel, Petra
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Taleghani, Kampiz Mansouri
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Pred. No. 6.6;
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                 80;
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                                                                                                                                                                                                              Length 2634;
                                                                                                                                                                                 Indels
2193
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RESULT 77

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RESULT 78
US-08-458-568A-11/c
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Best Local Similarity
"hes 77; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08458568A Patent No. 5821339
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LENGTH: 2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/341,550
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: PCT/US98/00840
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/035,955
PRIOR FILING DATE: 1997-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: SCR2177S
CURRENT APPLICATION NUMBER: US/09/613,182
CURRENT FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mayfield, Stephen
TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/069,400 PRIOR FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (197)..(2065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                       ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Infections
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    STREET: One LIVEL CITY: Philadelphia
                                  APPLICATION NUMBER: US/08 FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1004 CCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAG 1063
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                                                                                                                                                                                                                                                                                B: Woodcock, Washburn, Kurtz, Mackiewicz & No.
One Liberty Place, 46th floor
                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Compositions and Methods for Treatment of Herpesvirus
                                                                                                                                                                                                                                                                                                                                                    15
                                                         US/08/458,568A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB
Pred. No. 6.8;
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; LENGTH: 13842
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-30
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US-09-105-537-30
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                                                                                                                                                                                                                                                                                                                                  Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, I
APPLICANT: Liu, H.
                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 92; Conserv
                                                               Matches
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30,
                                                                                                                                                                                                                       APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
FULR APPLICATION NUMBER: US/09/105,537A
CURRENT FILLING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 568-343
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12001 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
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9891 GCGCGGCCGGCTCATGCAGGAGCTGCCCGCCGGTGGCGCGATGCTCGCCGTCCAGGCCGC 9950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649
                    440 GGGGAGCTGTTTTGGGAAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCCAGTCTG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            989 CTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCCGGGAC
                                                               87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCCCAGCCCCGCCCGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGA 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GC 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCCCTCCGCCTGCGCGTCACCGCGAGCACCTGGCGCGCCTGCGCCTGCGACGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCCTGCGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09105537A
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ilarity 50.5%;
Conservative
                                                               Conservative
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                                                                            2.4%;
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                                                               Score 37.8; DI
Pred. No. 13;
0; Mismatches
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Pred. No. 11;
0; Mismatches 9
                                                                                           DB 3;
                                                               82;
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                                                                                           Length 13842;
                                                                 Indels
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                                                                 Gaps
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BETLACH, Melanie C.

APPLICANT: BETLACH, Melanie C.

APPLICANT: BETLACH, Mary C.

APPLICANT: BETLACH, Mary C.

APPLICANT: McDANIEL, Robert

APPLICANT: McDANIEL, Robert

APPLICANT: TANG, Li

ITIE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE

FILE REFERENCE: 300622002120

CURRENT APPLICATION NUMBER: US/09/320,878A

CURRENT FILING DATE: 1998-05-27

EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER FILING DATE: 1998-05-06

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1997-04-30

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-09-08

EARLIER FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: 60/119,139

EARLIER APPLICATION NUMBER: 60/100,880

EARLIER APPLICATION NUMBER: 60/087,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Sti, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 36778
TYPE: DNA
OPCANION.
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US-09-105-537-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces venezuelae US-09-105-537-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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Best Local Similarity
Matches 87; Conserv
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Patent No. 6265202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%;
51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Pred. No. 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 36778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and pikromycin
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APPLICANT: ASSLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: MODANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
FILE REFERENCE: 300622002100
CURRENT APPLICATION NUMBER: US/09/141,908
CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 31
COPTWARE: DATE: 1998-05-28
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US-09-141-908-1
                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-141-908-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 38506
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SEQ ID NO 19
LENGTH: 38506
                                                                                                                                                                                                                                                                                       Query Match 2.4%; Score 37.8; Best Local Similarity 51.5%; Pred. No. 18 Matches 87; Conservative 0; Mismatche
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Streptomyces venezuelae
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                                                                                                                            500 CATGGGCGTCTTCTTGCCTGTGCCAGAAGAATGAGGACGACGAGTGTGCCGTGTGTCGGGACGG
                                                                                                                                                                                                                                      440 GGGGAGCTGTTTTGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 GGGGAGCTGTTTTGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTG 499
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                                                                                             GGAGGACGAGATCCGCGTGTGGCTGGAGACGGAGGAGCGGTACGCGGGACGTCTGGACGT
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CGCCGCCGTCAACGGCCCCGAGGCCGCCGTCCTGTCCGGCGACGCGGAC
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ilarity 51.5%;
Conservative (
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Sequence 1, Application US/09305640B
Patent No. 6255468
Patent No. 6255468
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham plc
TITLE OF INVENTION: No. 6255468e1 Compounds
FILE REFERENCE: GP30124
CURRENT APPLICATION NUMBER: US/09/305,640B
CURRENT FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2560
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; ORGANISM: Homo sapiens
US-09-305-640-1
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US-09-657-440-19
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; ORGANISM: Streptomyces venezuelae
US-09-657-440-19
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Patent No. 6509455
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                        Matches 118;
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Best Local Similarity
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CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 1999-05-27
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APPLICANT: BETLACH, Mei
APPLICANT: BETLACH, Mai
APPLICANT: McDANIEL, Ro
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                                    397 CAGGGCAGAGACTGGGGAGTTCAGGTACCCAGAGATGCTGCTGGGGGGAGCTGTTTTGGGA
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CCAGAATGGCGCAGAGGCCGGCGAACACCAGCCCCGACAGCAGGCACACCTCGCGCC
                                                                            CGGGACAGGCGCCGCCGGCCGCGACCGGGCCCAGGTACTTGAGGGCCAGCATAGCCG
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ilarity 46.8%;
Conservative
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                                                                                                                                                    Score 37.6; DB 3; Pred. No. 8.3; 0; Mismatches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 119
LENGTH: 2868
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed - NUMBER OF SEQ ID NOS: 550
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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254
                                                            AGCCCGGGGCAGGGAGGCCCCGCGCGCGCCCCCCGCGCAGCGGCTCACGTACTTGA 255
                                                                                                                           GGTTCCAGCGCGGCAGCCCGGACCGGGCCCCGGTGACGCTGCCGCAGCGCCCAACGGGA
                                                                                                                                                                                         CCAGAATGGCGCAGAGGCCGGCGAACACCAGCCGGACAGCAGGCACACCTCGCGCC 375
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                          CCAGTGGGACCT 648
                                                                                        GIGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCTCCGGGAGATCC 636
                                                                                                                                                        TGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGAGCTCATCTGCT
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Gurney, Austin L.
Sherwood, Steven
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Watanabe,Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stewart, Timothy A.
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243
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Pred. No. 8.6;
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RESULT 86 US-09-774-528-383/c

383, Application US/09774528 o. 6743619

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; LOCATION: (92)..(1309)
US-09-774-528-383
                                                                                                                                                                                                                                                                                                                                                9-09-252-991A-9715/c
Sequence 9715, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.4%; Score 37.4; DB 4; Best Local Similarity 50.9%; Pred. No. 8.1; Matches 89; Conservative 0; Mismatches 86;
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                                                                 SEQ ID NO 9715
                                                                                                                                                                                                                                                                                                        SENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                              FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Drmanac, Radoje T.
ITLE OF INVENTION: No. 6743619el Nucleic Acids
ITLE OF INVENTION: Polypeptides
ORGANISM: Pseudomonas aeruginosa
                                          ENGTH: 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1706
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Zhou, Ping
Zhou, Ping
Zhou, Ryle
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Wang, Dunrui
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Wehrman, Tom
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di, Vinod
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Patent No.
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Best Local Similarity
           TELEPAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2150 base pairs
TYPE: nucleic acid
STRANDEDNESS: signie
                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92.401.231.3
PILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
RETERRENCE/DOCKET NUMBER: 410.007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEIVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY O
TITLE OF INVENTION: IMMUNOLOGY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 661-8000
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MEDIUM TYPE: Floppy
                                                                                                                            TELEPHONE:
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STRANDEDNESS:
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Pred. No. 6
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US-09-428-711A-13/c
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                                                                                                                                                                                     SOFTWARE: Fas
SEQ ID NO 13
LENGTH: 3995
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09428711A Patent No. 6358720
Best Local Sim Matches 117;
             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Shirasawa, Mabdaki
APPLICANT: Shirasawa, Takuji
APPLICANT: Tokumitsu, Hiroshi
APPLICANT: No. 6359720uchi, Teruhisa
TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE
FILE REFERENCE: 06501-045001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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PRIOR FILING DATE: 1997-04-20

NUMBER OF SEQ ID NOS: 21

PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/428,711A CURRENT FILING DATE: 1999-10-28 PRIOR APPLICATION NUMBER: PCT/JP98/01246 PRIOR FILING DATE: 1998-03-23
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1997-04-28
                                                                   NAME/KEY: CDS
LOCATION: (388)...(3540)
NAME/KEY: misc_feature
LOCATION: (1)...(3995)
OOTHER INFORMATION: n = A,T,C
                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
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NAME/KEY:
LOCATION:
                                                                                                                                             FEATURE:
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ORGANISM: Hum
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   Conservative
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 0,
             Score 37.2;
Pred. No. 12
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 Mismatches 136;
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RESULT 91
US-09-839-479-28
; Sequence 28, Application
; Sequence 76727222
; Patent No. 6727222
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US-09-418-710-28
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; LOCATION: (346)...(4926)
US-09-418-710-28
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CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
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Best Local Similarity 53.4%;
Matches 78; Conservative
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Patent No. 6596482
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TYPE: DNA
ORGANISM: Homo
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
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GENERAL INFORMATION:
APPLICANT: JOSS, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002

US/09839479

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; LOCATION: (346)...(4938)
US-09-418-710-30
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SOFTWARE: FastSEQ fo
SEQ ID NO 30
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LENGTH: 5561
                                                                                       Query Match
Best Local
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Best Local (
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CURRENT FILING DATE: 199-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9
PRIOR FILING DATE: 1997-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPERENCE: 06501-042001
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
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CURRENT FILING DATE: 2001-04-20
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LOCATION: (346)...(4926)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                  FEATURE:
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 30
LENGTH: 5573
TYPE: DNA
ORGANISM: Homo sapiens
PAME/KEY: CDS
LOCATION: (346)...(4938)
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US-09-839-479-30
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                                                                                                                                                                                                                                                                                          US-08-146-930-1/c
                                                                                                                                                                                                                                                                                                           RESULT 94
                                                                                                                                                                                                                                                   Sequence 1, Application US/08146930 Patent No. 5958764
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Roop, D
APPLICANT: Rothnag
APPLICANT: Greenha
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 9/116570 PRIOR FILING DATE: 1997-04-18 NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                    TITLE OF INVENTION: SP
TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                            CITY: Los Angeles
STATE: California
                                                                      STREET:
               COUNTRY:
                                                                                       ADDRESSEB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 CCTTCCACCTGGCCTGCCCTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAGGT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 ACGAGTGTGCCGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGG 594
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90017
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                                                                    611 West Sixth
                                                                                                                                                            Rothnagel, Joseph A.
Greenhalgh, David A.
NVENTION: SPECIFIC EXPRESSION VECTORS
               U.S.A.
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                                                                                                                                                                                                                   Roop, Dennis R.
                                                                                     LYON & LYON
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                                                                                                                                           AND METHODS
                                                                      Street
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Pred. No. 13;
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RESULT 95
US-08-458-240-1/c
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                                                                                                                                      Sequence 1, Application US/08458240 Patent No. 6143727
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Best Local :
GENERAL INFORMATION:

APPLICANT: Roop, Dennis R.

APPLICANT: Rothnagel, Joseph A.

APPLICANT: Greenhalgh, David A.

TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 5958764 yet assigned (204/132)
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Pred. No. 14;
0; Mismatches 153;
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RESULT 96
PCT-US93-03993-1/c
; Sequence 1, Application PC/TUS9303993
; GENERAL INFORMATION:
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Best Local Similarity 47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYO
STREET: 611 West Sixt
CITY: Los Angeles
STATE: California
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
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STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                         GGCGGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCT 820
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Pred. No. 14
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Roop, Dennis R.

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RESULT 97
US-09-183-861-34/c
; Sequence 34, Application US/09183861
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NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713,651-5325
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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HYPOTHETICAL:
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LENGTH: 6530 base pairs
TYPE: NUCLEIC ACID
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
CORRESTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE EPIDERMAL
TITLE OF INVENTION: VECTOR SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19930. CLASSIFICATION:
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47.8%;
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Pred. No. 1
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Best Local S
Matches 184
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/183,861
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ORIGINAL SOURCE:
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LENGTH: 516 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICATION NUMBER: 09/0
FILING DATE: 12-FBB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
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APPLICANT: Campos-Neto,
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin
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ADDRESSEE: SEED and
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Skeiky, Yasir A.W.
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Best Local Similarity
Matches 184; Conserv
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Patent No. 6
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APPLICANT: Reed, Steven
APPLICANT: Campos-Neto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 516 base pairs
TYPE: nucleic acid
GTBANNEDURES. 4 double
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
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CORRESPONDENCE ADDRESS:
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APPLICANT: Skeiky, Yasir A.W.
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TOPOLOGY: lir
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CTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACC 1034
                                  CCACCTGTGCCTCCAGCTCGGCGCGCTGCTGCGGGGGGGTGTCTAGGCGCTGCTGCAGCT
                                                                    TCAGCAGAACCT--GGCTCCTGGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTG
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; TYPE: DNA
; ORCANISM: Leishmania major
US-09-551-974A-34
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; Sequence 34, Application US/09551974A
; Patent No. 6500437
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SEQ ID NO 34
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/551,974A
CURRENT FLING DATE: 2000-04-14
CURRENT FLING DATE: 101
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHN
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RESULT 100
US-09-565-501A-34/c
US-09-565-501A-34/c
; Sequence 34, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:

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APPLICANT: Reed, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Shatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Peter Probst
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121,420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LEISHMANIA major
US-09-565-501A-34

CORGANISM: Leishmania major
US-09-565-501A-34
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Search completed: February
Job time : 195 secs
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AL053013 Drosophi1
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/tissue_type="pooled germ cell tumors"
/lab_host="PH10B"
/clone_lib="NCI_CGAP_GC4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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1 (bases 1 to 1506)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera; S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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These sequences were made by sequencing genomic exons and on them based on alignment.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM6928"
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VERSION KEYWORDS SOURCE ORGANISM

Homo

sapiens (human) sapiens

RESULT 2 AY419550

DEFINITION ACCESSION

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1506 bp VIRTUAL

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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These sequences were made by
them based on alignment
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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found through the I.M.A.G.E. Consortium/LLNL
www-bio.llni.gov/bbrp/image/image.html
Insert Length: 701 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk,
                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 433)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                   Mus musculus
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                                                (bases 1 to 1512)
                                                                                                                musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_GC4"
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1257620"
/tissue_type="pooled germ
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD 20850, USA
These sequences were made by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene trios
Science 302 (5652), 1960-1963 (2003)
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Inferring nonneutral evolution from human-chimp-mouse
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM6928"
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Pred. No. 3.2e-53;
0; Mismatches 410;
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451 bp mRNA linear EST 24-AUG-200 uu49c07.yl Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:3375276 5' similar to TR:Q9Z0E3 Q9Z0E3 AIRE PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov)
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                                                                                    GTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCG
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                  CTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTC
                                                              GTGTGGCGATGGCACCGAGGTGTTGCGGTGTGCACACTGTGCCGCTTCCACTGGCG
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Location/Qualifiers
                                                                                                                           Conservative
                                                                                                                                                                                                   /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE:3375276"
                                                                                                                                          10.5%;
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                                                                                                                           0;
                                                                                                                         Score 162.6; DB 2
Pred. No. 5.5e-26;
0; Mismatches 84
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                                                                                                                                                                                                                                                                                                                        PUBMED
                                                                                                                                                                                                                                                                                                                                     NKS Okazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinicich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Numata, K., Okido, T., Pontius, J.U., Qi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yang, S., Pasawa, M., Yang, I., Yang, L., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y., Sasaki, K., Sasaki, D., Shibata, K., Shimadai, K., Shimadai, R., Sakazume, N., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1073
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                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY728790 RIKEN full-length enriched,
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BY728790.1
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
                                                                                             Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone C330016003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 632)
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l, ES cells Mus musculus
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FEATURES
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (200)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genome Sequences Mamm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit
                                                                                                                                                                                                                                                                                                                                    GTGAGCTCATCTGTTGTGACGGCTGTCCCCGGGCCTTCCACCTGGCTTGCCTGTCCCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGTGCCGTGTGTCGGGACGGCG
ACCAATCTCCGCTT-GCAATCCTGCTGCAGACTCGACTCCCACGCCAGGCACACCGGG
                                             TCCCCCCGGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAG
                                                                                                                                                  AGGAGGTGCAGCCCCGGGCAGAGGAGCCCCGGCCCCAGGAGCCACCCGTGGAGACCCCCGC
                                                                                                                                                                                                  CTCTGCAGGAGATCCCCAGTGGCCTCTGGAGATGCTCCTGCTGCCTCCAGGGCAGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="RIKEN full-length enriched, ES cells"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab
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/clone="C330016003"
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| host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 156.2; DB 6; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 104;
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FEATURES

Location/Qualifiers organism="Mus musculus'

source

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JOURNAL
PUBMED
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AUTHORS
TITLE
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Klausner, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkine, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsich, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Petere, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., García, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lux, Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouses cDNA seguences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 138 Row: 9 Column: 15 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                           Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (24-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus
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                                                                                                                                                                                                Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                     Nancy Liao
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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Best Local S
Matches 177
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177; Conserv
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                                                                                                                                                                                                                                                                                                   Other_ESTs: uu49c07.yl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE630816 511 bp mRNA linear EST 25-AUG-200 uu49c07.x1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3375276 3' Similar to TR:Q9Z0E3 Q9Z0E3 AIRE PROTEIN. ;, mENA
                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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EST.
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                                                                                                                                                                                                                                                       quality sequence stop: 391.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1282549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Thymus gland, mous
/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pT7T3-Pac"
                                                                                                            dev_stage="4 weeks"
                                                                                                                                                                                          mol_type="mRNA"
|strain="C57BL/6J"
                                                                                                                              tissue_type="Thymus"
                                                                                                                                                             clone="IMAGE:3375276"
                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                             xref="taxon:10090"
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    double-stranded cDNA was ligated to Eco RI adaptors
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Query Match
Best Local Similarity
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                                                                                                                             ATGACCTGGAGTCCCTTCTGAGCGAGCACCTTCGATGGCATCCTGCAGTGGGCCATCC 1245
                                                                                                                                                                                                             CCCCTGGGCCTGCCAA-----GGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGG
                                                                                                                                                                                                                                                          GACTCGACTCCACCGCGGGCACACCGGGNGAAGCTGTACCCACTTTTGGGCCCCCGTCCAG
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AGAGCATGTCACGCCCGCTGGCCGAGACACCACCCT
                                        AGAGCATGGCCGTCCGGCGGCCCCCTTCCCCTCCT
                                                                                ACGACCTGGAGTCCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCC
                                                                                                                                                                     CACCTGGGCTTGCCAAGGTAGGGGACGACTCTGCTAGTCACGACCCTGTTCTACATAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Pharmacia), digested with Not I and cloned into the Pand Eco RI sites of the modified pT773 vector. RNA provided by Dr. Bertrand Jordan. Library went through rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%;
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Pred. No. 2.1e-14;
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JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS DEFINITION ORGANISM source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 542)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.

The WashU-HHMI Mouse EST Project 542 bp mRNA linear EST 16 VX91507.r1 Soares thymus 2NbMT Mus musculus cDNA clone IMAGE:1282549 5' Similar to TR:015164 O15164 TRANSCRIPTION INTERMEDIARY FACTOR 1. ;, mXNA sequence. Unpublished (1996)
Contact: Warra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Ld Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wa Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 472. Location/Qualifiers MGI:674349 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information. Mus musculus AA866822 AA866822.1 Mus musculus (house mouse) Possible reversed clone: similarity on wrong strand /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:1282549" organism="Mus musculus" GI:2962267 Louis, 3 16-MAR-1998

58; 9,

9

Gaps

Length 420; Indels

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 420)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Pigott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Priddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Reyne,R., Potter,J.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Payne,R., Potter,J., Vogel,P., Walke,W., Xu,N.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Van Sligtenhorst,I., Vogel,P., Walke,W., Van Sligtenhorst,I., Vog
                                                                                                                                                                                                                                    Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence. CG513175 CG513175.1 GI:37299748
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OST66421 Mus musculus 129Sv/Ev 1
                                                                                                                                                                                                                                                                                                                                                Lexicon Genetics Incorporated 4000 Research Forest Drive, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                          Email: materials@lexgen.com
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/mol_type="genomic DNA"
                        /db_xref="taxon:10090"
/clone="OST66421"
                                                                                /mol_type="genomic DNA"
/etrain="129Sv/Ev"
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/dev_stage="4 weeks"
/lab_host="DH10B"
cell_type="embryonic stem cell"
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83.2%;
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Pred. No. 6.9e-10;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAF National Cancer Institute)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI552580 384 bp mRt vx26b07.x1 Soares_mammary_gland_NbMMG IMAGE:1265557 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is from the 3' end quality sequence stop: 381. Location/Qualifiers
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                                              T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NbMMG"
/notes="Organ: mammary gland; VecTor: pT7T3D-Pac
/pharmacial with a modified polylinker; Site 1: Not I.
Site_2: Eco RI; 1st strand cDNA was primed with a Not
                                                                                                                                                                                            /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:1265557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6J"
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Pred. No. 1.2e-09;
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                                                                                                                                                                                                                                                                                                                   source
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666 CTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCCCCGGGCCCCAGGAGCCA
                                                   136
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sgc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC endwas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG069825 947
Pan troglodytes DNA, clone: E
AG069825 AG069825.1 GI:16621627
GSS.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                   GCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGAACCTGGAGGTGCTCCAGCTGC
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R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                tracking errors.
                                                                                                                                                                                               /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-060I13.F"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                 'sex="male"
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77.6%;
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Pred. No. 1.1e-08;
0; Mismatches 30
                                                                                                                Score 73.4; DB 9;
Pred. No. 8.5e-06;
0; Mismatches 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., Toyoda, A., Taylor, T.D.,
and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 bp DNA linear GSS 03-NOV-200 PTB-060I13.F, genomic survey sequence.
                                                                                                                                                                                                  Male
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Teleosteti; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Roest Crollius,H., Jaillon,O., Dasilva,C., Bernot,A., Fizames,C., Wincker,P., Brottier Saurin,W. and Weissenbach,J. Estimate of human gene number provided by cusing Tetracdon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Brottier,P., Quetie
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                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                          CNS0091P 925 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Submitted (02-JUN-1999) Genoscope
BP 191 91006 EVRY cedex - FRANCE (
- Web : www.genoscope.cns.fr)
                                                                                                                                                                             fly), genomic survey sequence.
AL053013
AL053013.1 GI:4934461
GSS.
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/note="Genoscope sequence ID : C0BG022BH08SP1-end
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/mal_type="genomic DNA"
/db xrefe="taxon:99883"
/clone="022016"
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Pred. No. 1.1e-05;
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(E-mail : segref@genoscope.cns.fr
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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UI-E-EJ0-aii-m-23-0-UI 3', mRNA sequence.
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 674)

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to fac
Genome Res. 6 (9),
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|/clone="BACR19D16"
|/clone_lib="RPCI-98"
|/note="end : TET3"
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13.5%; Pred. No. 6.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 FORWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bento-soares@uiowa.edu
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                                                                                                                                                                                                                           GGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGT
                                                                                                                                                                                                                                                                                                                          CATCCTGTGCGACACCTGCCCGAGGGCCTACCATCTCGTGTGCCTGGACCCAGAGCTGGA 522
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                                                                                                                                                                                GAAGGCTCCCGAGGCAAGTGGAGCTGCCCCCACTGTGAGAAGGAGGGGGATCCAGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Clone lib="UI-E-EXO" / Clone lib="UI-E-EXO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_TISSUE=human fetal eyes
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/tissue_type="fetal eyes, lens, eye anterior segment,
optic_nerve, retina, Retina Foveal and Macular, RPE and
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Fax: 319 335 9565
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375 Newton Road , 4156
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="UI"-E-EJO-aii-m-23-0-UI"
/tissue type="fetal eyes, lens, eye anterior segment,
/tissue type="fetal eyes, lens, eye and Macular, RPE a
cptic nerve, retina, Retina Foveal and Macular, RPE a
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CR566920
5', mRNA
                                                                                                                                                                                                                                                                                                                97;
   AQ474914 350
CITBI-E1-2591L22.TF CITBI-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: THdA010e06.plkbSP6
This sequence is from a Xenopus Gene Collecconstructed by Nigel Garrett.
Seq primer: SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Silurana.

(Dases 1 to 940)

Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,
Sanger Xenopus tropicalis EST project 2001 (2004)

Unpublished (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR566920.1 GI:50396997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus tropicalis (western clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G 692
                                                                                                                                                                                                                                                                TGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGT
                                                                                                                                         AGTGGGACCTGGAGGTGCTCCAGCTGC 665
                                                                                                                                                                                                           GACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTTCCCCTCCGCTCCGGGAGATCCCC 638
                                                                                                                                                                                                                                            GGCTCCCGAGGGCAAGTGGAGCTGCCCCCCACTGTGAGAAGGAGGGGGATCCAGTGGGAGCC
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                                                                                                        AGCGGCACATGGAGATGTGATACTTGC 391
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                              /clone="THdA010e06"
/dev gtage="tailbud head (gtage 28-30)"
/dev gtage="tailbud head (gtage 28-30)"
/lab_nost="Bscherichia coli DH10B."
/clone_lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from tailbud head. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                               4.3%;
                                                                                                                                                                                                                                                                                                             Score 67; DB 7; Length 940; Pred. No. 0.00024; 0; Mismatches 50; Indels
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Xenopus tropicalis cDNA clone THdA010e06
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 sapiens
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                   DNA
linear
genomic
   GSS
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   23-APR-1999
2591L22,
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                                                                                      REFERENCE
AUTHORS
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ORGANISM
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VERSION
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AV591350
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Best Local Similarity
Matches 68; Conserv
     JOURNAL
                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1145 CAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGGATGACCTGGAGGTCCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                     1205 GAGCGAGCACAC 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Other GSSs: CITBI-E1-2591L22.TR
Other GSSs: CITBI-E1
Contact: Shaying Zhao, William Nierman, M
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                     169
                                                                                                                                                                                                                                            AV591350 5
AV591350 Bos taurus brain 5', mRNA sequence.
AV591350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 350) Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence AQ474914 AQ474914.1 GI:4657033 GSS.
                                    Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                    Takasuga, A., Hi and Sugimoto, Y.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
                                                                                                                                                                         Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                   bovine ESTs
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                                                                                                                                                                                                                                                                                                                                                                                     GAGCGAGGTAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCTTCT
                                                                                                      (bases 1 to 563)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
     Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CITBI-E1"
/note="Vector: pBeloBAC11;
CalTech Human BAC Library !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2591L22"
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                                                                                                                                                                                                                             GI:9702343
                                                                                    Hirotsune, S., Itoh, R., Jitohzono, A.,
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Pred. No. 0.00044;
0; Mismatches 4;
   (22),
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     E108 (2001)
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                                                                                        Suzuki, H.,
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PUBMED
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACCGGCTGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
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11713328
                                                                                                                                         Analysis of bovine mammary gland EST the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                            1 (bases 1 to 610)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
                                                  Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                             610 bp
197111 BARC 5BOV Bos taurus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing.
This clone was obtained from a
Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                        Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-248-25-5725
                                                                                                         12140684
                                                                                                                                                                                               and Quackenbush,J.
                                                                                                                                                                                                                                                                   Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCTACCACATCCACTGTCTGAACCCCCCCCCCCGACATCCCCCAACGGCGAATGGCT
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                301 504 8416
301 504 8414
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9913"
/clone="E1BR018A07"
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                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Pred. No. 0.00064;
0; Mismatches 95
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5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.2%;
Best Local Similarity 62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                HITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT 21860720 XtSt10-30 Xenopus IMAGE:7097432 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                              National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1. (bases 1 to 587)
                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14930 row: k column: 22
                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CN322716.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 117 row: I column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and -minmatch 12 options.
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus tropicalis (western clawed frog
                                                                                                                                                          cDNA Library Preparation: Wei Wu, DKFZ
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAG
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                         quality sequence stop: 587.
Location/Qualifiers
1..587
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/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and dises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .610
organism="Xenopus tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:46380352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 2;
Pred. No. 0.00064;
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL106054
AL106054.1 GI:5619805
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS015Y4 linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCAAAGTTTTCCACCTGTCGTGCCACGTGCCTACACTGATGAACTTTCCCAGTGGTGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCCTCCGGGAGATCCCCAGTGGGACC
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/db xref="taxon:8364"
/clone="IMAGE:7092432"
/tissue type="whole embryo, pool of stages 10, 20 and 30"
/tissue type="whole embryo, pool of stages 10, 20 and 30"
/clone_Iib="XtSt10-30"
/note="Vector: pRKW2; Site_1: BamH1; Site_2: XhoI; 10 ug
of polyA+ RNA was isolated from a mixture of embryos at
stage 10, 20 and 30 and primed by oligo-dT primer:
5'-GACAGACAAGCATCC(T)167N-3' (where V=G,A,C).
5-methyl-dCTP was used instead of dCTP in the first-strand
synthesis in order to get hemimethylated cDNA. After
full-length enrichment, oligo-dG tailing and normalization
against itself, second-strand synthesis was carried out by
priming with 5'-GACAGACACCTCGAGTTAATTAAT(C)13-3' dsDNA
was digested with XhoI/BamHI and directionally cloned into
the pRKW2 vector. Average insert size is 1.5 kb. Library
constructed using the Carninci protocol (Genome Research
2000) by Drs. W. Wu and C. Niehrs (DKFZ, Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
                                                                                                                                            Location/Qualifiers
                                               /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                               organism="Drosophila melanogaster"
                           clone="BACN15E10"
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Pred. No. 0.00097;
0; Mismatches 63;
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AUTHORS
TITLE
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VERSION
KEYWORDS
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CK704772/c
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
E 1 (bases 1 to 807)
E 1 (bases 1 to 807)
S Wei.C., Mathavan,S., Thoreau,H., Lim,L., Lee,C. and Ruan
Genome Institute of Singapore, Zebrafish Gene Collection
L Unpublished (2004)
Contact: Ruan Y
Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
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                                             Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00008-BR2_
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK704772 807 bp n
ZF101-P00008-DEPE-R_E20 GISZF001_ra
IMAGE:7137214 3', mRNA sequence.
FORWARD: M13
BACKWARD: M13
                                                                                                                   Tel: +65 6478 8073
Fax: +65 6478 9059
                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CK704772.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGSGGGGSSGGGGGVGGCGVMGGGGGGGGGCCCSSGSGGGGGMSGMSNMGGGGGGMSS
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/note="end : T7"
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rerio cDNA
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1121 1096 1061 1036 1001 976 941 916 881 856 821 796 761 736 701

RESULT 23 CNS015Y4

DEFINITION

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238

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178

Query Match Best Local S Matches 102

102;

REFERENCE AUTHORS TITLE

JOURNAL

Euteleostomi;

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EST 30-MAR-2004 A clone

SOURCE ORGANISM

VERSION ACCESSION **ŒYWORDS**

COMMENT

FEATURES

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JOURNAL
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Best Local Similarity
    AUTHORS
                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                              644 GACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTG 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          524 GAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGG
                                                                                                                                                                                                                    Pan troglodytes DNA, clone: PTB-003A10.F, genomic AG030591
AG030591.1 GI:16557464
GSS.
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                                                                               Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                Pan troglodytes (chimpanzee)
Pan troglodytes
Fujiyama, A., Hattori, M.,
                                       Unpublished
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                           TACCTGGAGCTGCCCACACTGCGAGAAGATGGGAATCCAGTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTCCACGGGCCTATCACATGGTCTGCTTGGACCCCGACATGGAGAAGGCCCCTGAGGG
                  (bases 1 to 888)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linker/adaptor sequence: same as the priming sequence; Average insert size: 2kb; For FCR insert analysis: Use M13 Forward and reverse primers; Library Amplified; Recombinants (inserts): 98%; Library complexity: 5x106; Full-length construction (method): SMART, a Clontech method The pooled tissue RNA was collected and used to construct full length enriched cDNA library and also served as template to synthesize complex first strand cDNA probe. Two high density colony arrays were made from over intensity clones and hybridized with the probes. Low intensity clones were selected as they represented rare expressed clones. The hybridization intensities for all clones span from 0 to 1.8 million counts and the low abundant class ranged from 0 to 13,000."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.ATTCTÁGAGGCGÁGGCGGCCGACATG(T)30VN; Directionally cloned, 5 cloning site: Sfi A site GGCCATACGGCCC; linker/adaptor sequence: 5.AAGCAGTGGTATCAACGCAGAGTGGCC; 3', cloning site: Sfi B site GGCCGAGGCGGCC; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GISZF001_ra"
/note="Vector: pDNR-LIB, Site_1: Sfi A (GGCCATTACGGCC);
/site_2: Sfi B (GGCCGAGGCGGCC); Priming method: Sfi-(dr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Embryo"
/dev_stage="7 Different embryonic Stages(From just
/ertilized Embryos to 72 hours just hatched baby fish)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Singapore local
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.6; DB 7; Length 807; Pred. No. 0.0014; o; Mismatches 64; Indels
Toyoda, A., Taylor, T.D., Yada, T.,
                                                                                                  Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method: Sfi-(dT)30
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Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (R-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing: -21M13
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                                                                                                                                                                                                                                                              CCCAGCCCGCCCGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCC 1172
                                                                                                                                                                                                                                                                                                                                                                                      GACTCCTCGGCCCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCT 932
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DN/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="PTB-003A10.F"
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Pred. No. 0.0014;
0; Mismatches 335,
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AUTHORS
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Matches 100; Conserv
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vn94e11.rl Stratagene mouse heart
IMAGE:1039628 5', mRNA sequence.
AA792266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: toseer@toulouse.inra.fr

Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
Contact: Tosser-Klopp G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX915120.1 GI:41131899
EST.
Sus scrofa (pig)
Sus scrofa
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BX915120 Sus Scrofa library (scan) S
scan0028d.a.12 Sprim, mRNA sequence.
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Chemin de Borde-Rouge -
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 783)
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                                                                                                                                                                                             TGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTG 689
                                                                                                                                                                                                                                       CCCAAAGTATTCCACCTGTCTTGTCACGTGCCCACGCTGGCAAATTTTTCCGAGTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9823"
/clone="scan0028d.a.l2"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_libb="Sus Scrofa library (scan)"
/clone_libb="Sus Scrofa library (scan)"
/clone_libb="Sus Scrofa library (scan)"
/note="tissues: adipose tissue, brain, kidney, liver,
muscle_ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Sus scrofa"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                  4.18;
61.78;
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Pred. No. 0.0015;
0; Mismatches 62;
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Auzeville
                                       mRNA linear EST 09-FEB-1998 (#937316) Mus musculus cDNA clone
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BP27, 31326
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ofa cDNA clone
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                                                         EST 09-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ORGANISM

Mus musculus Mus musculus CF161888.1 EST.

GI:33271437 (house mouse

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ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                  RESULT 28
CF161888
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AUTHORS
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Best Local S
Matches 89
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                                                                                                             CP161888 485 bp mRNA linear EST 25-JUL-2003 B0703E06-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long) Mus musculus cDNA clone NIA:B0703E06 IMAGE:30458165 5', mRNA sequence. CP161888
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1 (bases 1 to 406)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
Contact: Marra M/Mouse EST Project
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EST.
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Fax: 314 286 1810
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/dey stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/lab_lost="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone_Torgan: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1: heart; Vector: pBluescript SK-; Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:1039628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="NIH Swiss"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.1%; Score 63.2; DB 1; 67.4%; Pred. No. 0.0016; tive 0; Mismatches 43;
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                                    593 GGCCTTCCACCTGGCCTGCCTGCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG
115 TTCCTACCACATCCACTGCCTGAACCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT 174
                                                                                                                      5
                                                                                                                                                                                                                                                      89;
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0703 row: E column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 485)
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                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                  GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGAGCTCCTGTGCTGTGACACATGCCCTTC 114
                                                                                                                                                                                                                                               Conservative
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/note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
/note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
/note="vector: pCMV-SPORT6 (Invitrogen); Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were obtained from Dr.Mark G. Carter (NIH/NIA-IRP).
EG cells were cultured at 37. C, 5% CO2 in DMEM
supplemented with 15% ES cell-qualified FBS, 0.1mM
non-essential amino acids, 2 mM glutamine,
penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM
beta-mercaptoethanol, and 10000000 units of LIP per liter.
Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                             to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 4.0 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
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(Long)"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                             Score 63.2; DB 6; Pred. No. 0.0016;
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                                                                                                                                                                                                                                                                                                              Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: B0181 row: H column: 02 Seq primer: -2ML13 Reverse High quality sequence stop: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA893864 514 bp mRNA
B0181H02-5N NIA Mouse Neural Stem Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Ko,M.S.H.
Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piao,Y., Dudekula,D.B., Qian,Y., Martin,P.R., Aiba,K., Vescovi,A.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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/dev_stage="Adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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Score 63.2; DB 6;
Pred. No. 0.0016;
                Length 514;
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute on Aging/National Institutes of Health 33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov Plate: K0332 row: G column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 562)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Umezawa, A. and Ko, M.S.H.
Umezawa, A. and Ko, M.S.H.
Tystematic Analyses of NIA Mouse Osteoblast cDNA Library (Long)
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CA564994.1 GI:25109673
EST.
Mus musculus (house mous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
Other_ESTs: K0332G02-3
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA564994 562 bp mRNA linear EST 19-NOV-200 K0332G02-5N NIA Mouse Osteoblast cDNA Library (Long) Mus musculus cDNA clone NIA:K0332G02 IMAGE:30057385 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACGAGTGTGCCGTGTCTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG
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quality sequence stop: 562
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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(clone="NIA:K0332G02 IMAGE:30057385"
/tissue_type="Osteoblast"
/cell_line="KUSA-A1 cells"
                                                                                                                                                                                                                                                                                                                               lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                           'strain="C3H/He"
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Local 653 GTGCTCCAGCTG 664 593 GGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG 533 GGACGAGTGTGCCGTGTCGGGGGACGCCGATCTGCTGTGACGGCTGCCCTCG Similarity CTGTCCCCGCTG 204 TTCCTACCACATCCACTGCCTGAACCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGGAGCTCCTGTGCTGTGACACATGCCCTTC Conservative The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao (NIA)." 4.1%; 0 Score .63.2; DB 6 Pred. No. 0.0016; Mismatches 6; 43; Length Indels 0 652 132 592 192

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 564)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki BB654405
BB654405 RIKEN full-length enriched, 2 days neonate thymus thymic colls Mus musculus cDNA clone C920008E20 5', mRNA sequence. Mus musculus Mus musculus (house mouse) BB654405.1 GI:16488233

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj Tel: 81-45-503-9222 Fax: 81-45-503-9216 230-0045, Japan

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. .10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., and Hayashizaki,Y. Inoue, Y., Kira, A.

384 multicapillary sequencer. Genome Res.

sequencing pipeline with 384 multicapillary sequencer. Genome R 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,

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RESULT 32
CD551263
LOCUS
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AUTHORS
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Matches 89
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EST.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                            Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0325 row: H column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 604)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD551263 604 bp mRNA linear B0325H01-5 NIA Mouse E9.5 Whole Embryo cDNA Library musculus cDNA clone NIA:B0325H01 IMAGE:30431508 5',
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e mouse tissues
                                                                                                                                                                                                               Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                             Contact: Dawood B. Dudekula
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/cell type="thymic cells"
/dev_Etage="2 days neonate"
/clone_lib="RIKEN full-length enriched, 2 days neonate
thymus_thymic_cells"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:B0325H01-5"
/db_xref="taxon:10090"
/clone="NIA:B0325H01 IMAGE:30431508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                       organism="Mus musculus"
                                                                                                                                               ocation/Qualifiers
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Pred. No. 0.0016;
0; Mismatches 43;
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RESULT 33
CK781630
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 GGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin Unive
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK781630 625 bp mRNA UI-M-HEO-clz-o-ll-0-UI.rl NIH_BMAP_HEO Mus IMAGE:30630778 5', mRNA sequence.
                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 625)
                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGAGCTCCTGTGCTGTGACACATGCCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and purified by ethanol precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0kb. The library was constructed by Yulan Piao."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="E9.5 whole embryo"
/dev_stage="whole embryo includir
at 9.5-days postcoitum"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from6.1 ug of total RNA, treated with T4 DNA polymerase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone lib="NIA Mouse E9.5 Whole Embryo cDNA Library (Long)"
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Pred. No. 0.0016;
0; Mismatches 43;
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                                                                                                                                                                                                                                                                      Gene
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CDNA clone
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ORIGIN

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clone was contributed by the Brain Molecular Anatomy Project

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AUTHORS
TITLE
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LOCUS
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                                                                                                                                                                                                                                                                                                                                 634 bp
UI-M-FOO-caa-i-10-0-UI.r1 NIH BM
IMAGE:6408657 5', mRNA sequence
BU705998
             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 634)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                             BU705998
BU705998.1 GI:23636034
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Seq primer:
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/db_xref="taxon:10090"
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AUTHORS
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BU055310
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Best Local S
Matches 89
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ### 635 bp UI-M-F00-bzp-b-16-0-UI.r1 NIH BW IMAGE:6405423 5', mRNA sequence.
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                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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/dev_stage="embryo 12.5dpc"
/lab_host="PH108 (TI phage resistant)"
/clone_lib="NIH_BMAP_FOO"
/clone_lib="NIH_BMAP_FOO"
/clone_lib="NIH_BMAP_FOO"
/note="Organ: Brain; Vector: pXX- Asc; Site_1: Rcor I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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Pred. No. 0.0016;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                           CB246896.1 GI:28368540 EST.
Mus musculus (house mouse)
                        found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB246896
UI-M-FIO-cdy-k-21-0-UI.rl NIH_
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                                                                                                                                                                                                                                            Unpublished (1999)
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clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGACAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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/lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/inote="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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/strain="C57BL/6"
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Pred. No. 0.0016;
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CF726532
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                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 730)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UI-M-HB0-ckh-h-09-0-UI.r1 NIH_BMA
IMAGE:30547664 5', mRNA sequence.
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Seq primer: pYX-5.
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                                                                           This clone was contributed by the Brain Molecular Anatomy Project
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//lab_host="DH10B (T1 phage resistant)"
//clone_lib="NIH_BMAP_F10"
//clone_lib="NIH_BMAP_III"
//clon
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VERSION
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AUTHORS
TITLE
JOURNAL
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CN534827
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                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefi.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-M-HS0-cqd-k-04-0-UI.rl NIH_BMAP_HS0 Mus musculus cDNA clone IMAGE:30674835 '5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN534827
CN534827.1 GI:46862983
EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Seq primer: pYX-5.
Location/Qualifiers
1. .736
                                                                                        This clone was contributed by the Brain Molecular Anatomy Project
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/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
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/cloine=lib="NIH_BMAP_HB0"
/cloine="Torgan: Eye; Vector: pyx- Asc; Site 1: Bcor I;
/note="Torgan: Eye; Vector: pyx- Asc; Site 1: Bcor I;
/note="Torgan: Eye; Vector: pyx- Asc; Site 1: Bcor I;
/site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mENA size fraction, ligated
with EcoR I adaptor , digested with Not1 and then cloned
directionally into pyx-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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/mol_type="mRNA"
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Pred. No. 0.0017;
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CO045219
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106 TTCTTACCACATCCACTGCCTGAACCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT 165
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                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 754)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                   Seq primer: pYX-5.
Location/Qualifiers
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EST.
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/clone lib="NIH BMAP HS0"
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/note="Organ: Upper Head; Vector: pX-Asc; Site_1: PX-Book
/note="Organ: Upper Head; Vector: The libary tag
/note="Organ: Upper Head; Vector: Upp
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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
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EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               755 bp mRNA UI-M-HOO-cqb-j-11-0-UI.rl NIH_BMAP_HOO Mus IMAGE 10664450 5', mRNA sequence.
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                                                                                                                                                                                                                 clone was contributed by the Brain Molecular Anatomy Project
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="t^"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Upper Head"
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/lab_host="DH10B (T1 phage resistant)"
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/clone_lib="NHH_BMAP_HO0"
/note="Organ: Head; Vector: pXx-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soarss, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
                                                                                 organism="Mus musculus"
                                                                                                                                  Location/Qualifiers
          xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63.2; DB 7; Length 754; Pred. No. 0.0017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus
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CA327845
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                                                                                                                                                                            FEATURES
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Best Local Similarity
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                                                                                                                                                 source
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
El (bases 1: / 762)
NIH-McC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC Clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 GGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCCAGTGGGACCTGGAG 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA327845 762 bp mRNA linear UI-M-FY0-ccw-f-03-0-UI.rl NIH BMAP_FY0 Mus musculus IMAGE:6825316 5', mRNA sequence.
CA327845 CA327845.1 GI:24545943
                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/lab_host="DhP10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP HOO"
/clone lib="NIH BMAP HOO"
/note="Oxgan: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6825316"
                                                                                                                                                                               location/Qualifiers
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Pred. No. 0.0017;
0; Mismatches 4
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CA749488
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGACGCTCATCTGCTGTGACGGCTGCCCTCG 592
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                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consorthum/LLML at:
http://image.llnl.gov
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CA749488.1 GI:25571583
EST.
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UI-M-FYO-cdd-n-01-0-UI.rl NIH_BMAP_FYO Mus
IMAGE:6831650 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                        Seq primer: pYX-5
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="DH10B (T1 phage resistant)"
/clome_lib="NIH_BMAP_FYO"
/clome_lib="NIH_BMAP_FYO"
/clome_lib="NIH_BMAP_FYO"
/clome_lib="NIH_BMAP_FYO"
/note="COrgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="COrgan: Brain; Vector: pYX- Asc
/primer containing a Not I site. Double strand cDNA was
/size selected according to mRNA size fraction, ligated
/with EcoR I adaptor, digested with NotI and then cloned
/directionally into pYX- Asc vector. The library tag
//sequence located between the Not I site and the polyA tail
//s AGCGAGACAG. This library was created for the University
//owa Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Discovery in the
//oward Brain Anatomy Project (BMAP): 'Gene Brain Anatomy Project (BMAP): '
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/db_xref="taxon:10090"
/clone="IMAGE:6831650"
                                                      /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                             Location/Qualifiers
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Pred. No. 0.0017;
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musculus
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CK637900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 GGCCTTCCACCTGGCCTGTCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG 652
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                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 787)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UI-M-HOO-cnt-m-12-0-UI.r1 NIH_BMAP_HOO
IMAGB:30642251 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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Similarity 67.48;
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                                                                                                                                                                                                                                                                                                   primer: pYX-5
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                                                                                                                                                                                                                                                                                                                                                                                       clone was
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                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="whole brain"
                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                       contributed by the Brain Molecular Anatomy Project
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Pred. No. 0.0017;
0; Mismatches 4
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musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa
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CDNA clone
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                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M. A.G.B. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CA752497.1 GI:25583236
EST.
Mus musculus (house mouse)
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UI-M-FO0-cdo-p-13-0-UI.r1 NIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE: 6831326
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/lab_host="PH108 (TI phage resistant)"
/clome_lib="Nufl_BMAP_HOO"
/clome_lib="Nufl_BMAP_HOO"
/note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                 clone was contributed by the Brain Molecular Anatomy Project
                                                                                                               /mol
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/tissue_type="whole brain"
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                                                                  db_xref="taxon:10090"
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No. 0.0017;
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AUTHORS
TITLE
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VERSION
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RESULT 44 CA752497

Ś 밁 Ś 밁 S ORIGIN

Matches

REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

FEATURES

source

/dev_stage="embryo 12.5dpc"

SOURCE ORGANISM

CEYWORDS

ACCESSION VERSION

DEFINITION

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Query Match
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                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UI-M-FIO-byu-a-09-0-UI.r1 NIH_BMAP_FIO N
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/clome lib="NNH BMAP FOO"
/note="Organ: Brain; "Vector: pXX- Asc; Site_1: EcoR I;
/note="Organ: Brain; "Vector: pXX- Asc; Site_1: Roc I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                                                                                                                                             clone was contributed by the Brain Molecular Anatomy Project
/db_xref="taxon:10090"
/clone="IMAGE:5702288"
/tissue_type="whole brain"
                                                                                                                                     /organism="Mus musculus"
                                                                                     strain="C57BL/6"
                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                . 832
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                                                                                                             type="mRNA"
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Pred. No. 0.0017;
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musculus
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Best Local Similarity
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AGENCOURT 8750481 NIH MGC 130 Mu
5', mRNA Bequence.
BU152563
BU152563.1 GI:22666095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                                                                                                                                                                                                                      High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                           Plate: LLAM13791 row: m column:
                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIGICCCCCCTG
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/clone libs"NIH_BMAP_FIO"
/notes="Organ: Brain; 'Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaido, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
  /lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_130"
/note="Organ: otocysts; Vector: pCM
                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6333110"
                                                                                                                                                                                                                                      ocation/Qualifiers
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Pred. No. 0.0017;
0; Mismatches 4
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Vector: pCMV-SPORT6.1; Site_1:
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BU152563

RESULT 46

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875 CTCCTCGGCCCTGCACCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCC

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RESULT 47
CNS006XK
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Matches
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TITLE
                                            Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                        source
                    Local
                                                                                                                                                                                                                                                                                                          Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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  120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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AL066051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                       Similarity
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                                                                                                                                                                      /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic ZOA"
/db_xref="raxon:7227"
/clone="BACR14N09"
                                                                                                                    /note="end : T7"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                 /clone_lib="RPCI-98"
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                    4.1%;
97;
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                    Score 63.2; DB 9;
Pred. No. 0.0017;
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Pred. No. 0.0017;
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Mismatches
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survey sequence T7 end of BAC #
189;
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                                            Length 935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR715927 1066 bp Tetracodon nigroviridis full-length CR715927 CR715927.1 GI:51214161 HTC; cDNA; full-length; Tetracodon r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                    AAGTGTCCACCAATGAAGGGGAAAGTTCAGAAAGTTTTAACTTGGCGATGGGGGGACCCA
                                                                                                                                     GCCTGCCTGTCCCCTCCGCGCGGGGGGTCCCCAGTGGGACCTGGAGGTGCTCCAGCTGC
                                                                                                                                                                              GTGTGCAAGGATGGAGGAGAGCTGTTGTGCTGTGACACCTGCCCCCTCCTACCACATC
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                                                        CTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCGGCCCCAGGAGCCA
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                         tissue_type="Eggs"
                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:47144"
                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Tetraodon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                              4.1%;
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                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK034549 array alinear HTC 03-APR-2004 mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430004K15 product:CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTONATIGEN 218 KDA PROTEIN) (MI2-BETA) homolog [Homo sapiens],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Submitted (16-JUL-2001) Yoshihide Hayashizaki,
                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RIKEN Genome Exploration Research Group Phase
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ency full-length cDNA
ol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      II Team and
                                                                                                                      Sakazume, N.,
                                                                                                                                                                                                                                                             Carninci, P.
                                                                                                                                         Ohsato, N.,
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Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
Please visit our web site for further details.
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                                                                                                                                                                 GGCCTTCCACCTGGCCTGCCGTCCGCTCCGGGAGATCCCCCAGTGGGACCTGGAG
                                                                 GTGCTCCAGCTG
                                                                                                                               TTCCTACCACATCCACTGCCTGAACCCCCCCCCCGCTGCCAGAGATCCCCAAACGGCGAATGGCT
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CTGTCCCCGCTG
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PKELLEGREEROF TVKNOGMS YNHCSWYSELOLELH-COVHERNYORKNUNDEPPSCOPE
GDEEKSRKKRINGD KFALEMEERFYRYGI KFEMMIHR ILMS VDKKGHVHYLI KWRDL
PYDOASWESEDVEI ODYDLFKOSYWHRELMTGSEGREGREKKLKKYLRKLERPETT
VDPTVKYEROPEYLDATGGTIHFYOMEGLAWLARSWAQGTOTTILADEMGLGKTVOTAV
FLYSLYKEGHS KGPFLVSAPLSTI INWEREFEMMAPDMYVVTYVGDKOSALI IRENEF
SFEDNAI IRGGKKASRMKKEASVKFHVLLTSYELLTIDMAILGS IDMACLI VDEAHRLK
NNOSKFFRULNGYSLOHKLLTGTFLONNLEELFHLANFLTPERRHNLEGFLEERADI
AKEDOI KKLHDMLGPHMLRRLKADVFKNMPSKTELI VRVELS PMOKKYYKY ILTRNFE
ALMARGGGNOYSLLNVMDLKKCONHFYLFEVAAMEAPKWPNGWTOSALI RASGKLL
LLOKMLKNLKEGGHRVLI FSOMTKMLDLEDFLEHEGYKYER IDGGITGMWROBA TOR
FNAPGAQOFCFLLSTRAGGLGINLATADTVI I YDSDWNPHNDIOAFSRAHRIGONKKV
MIYRFVTRASVEER ITQVAKKKOMLTHLVVRPGLGSKTGSMSKOELDDILKFGTEELF
KDBATDGGGDNKEGEDSSVIHYDDKAI ERLLDRNQDETEDTELOGMNEYLSSFKVAQY
KORSTONGSONSKOELDDILKFGTEELF
KDBATDGGGDNKEGEDSSVIHYDDKAI ERLLDRNQDETEDTELOGMNEYLSSFKVAQY
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HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN
218 KDA PROTEIN) (MI2-BETA) homolog [Homo sapiens]
(SWISSPROT Q14839, evidence: FASTY, 99.8%ID, 54.6%length,
match=3135)
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EVTAVDGYETDHQDYCEVCQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCE
KEGIQWEAKEDNSEGEEILEEVGGDPEEEDDHHMEFCRVCKDGGELLCCDTCPSSYHI
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/dev_stage="12 days embryo"
<1. .->3137
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/protein_id="BAC28749.1"
/db_xref="GI:26330021"
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/mol_type="mRNA"
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_xref="taxon:10090"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
616 SVSASSGMSSSVSSSGGRSSGSGGGGGGGGGGSGSGSGSGGSGGSGSVCSCSSGCMCRCSC
                                                                                                                                           676 CAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCGGCCCCAGGAGCCACCCGTGGAGA
                                                                                                                                                                                             736 ASSSSSCSSSVSCSSVASSMSCSSBSSSSSASSSSSSSSSSSSSSSSSCASCSCCCTSWSCSCST
                                                                                                                                                                                                                                           556 ACGGCGGGGAGCTCATCTGCTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGT
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AL053013.1 GI
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo:
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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                                                                                               TCTGCATGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGG
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/mol type="genomic DNA"
/db_rref="taxon:7227"
/clone="BACRI9D16"
/clone_ib="RPCI-98"
/note="end : TET3"
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survey sequence TET3 end of BAC #
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Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Boperson, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McWaterston, R. and Wilson, R. Waterston, R. and Wilson, R. WashU Xenopus EST project, 1999
Unpublished (1999)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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GRC pCS107 tropicalis St10-12 Xenopus dad29408.yl Wellcome CRC pCS107 tropicalis St10-12 Xenopus tropicalis cDNA clone IMAGE:4440999 5' similar to TR:095884 095854

TRANSCRIPTIONAL INTERMEDIARY FACTOR 1 ALPHA. ; mRNA sequence.
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Library constructed by A. Zorn and J. Mason (Wellcome/CRC
Library constructed by A. Zorn and J. Mason (Wellcome/CRC
Library Control of the Cont
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1 (bases 1 to 587)
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                                                                                   TGGATCTGCACCTTTTGCCGGGACCTGTCCAGACCAGAAGTGGAG
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/tissue_type="whole embryo, stages 10-12"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome_CRC_pCS107 tropicalis_St10-12"
/clone_wellcome_CRC_pCS107; Site_1: NotI; Site_2: EcoRI; CDNAs_were_oligo-dT_primed_and_directionally_cloned_Average_insert_size_1.5 kb, range_0.5-4 kb. Library_constructed_by_A. Zorn_and_J. Mason_(Wellcome/CRC_Institute). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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Pred. No. 0.0022;
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Matches 88
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                                                                                                                                              593 GGCCTTCCACCTGGCCTGCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG
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626 CTGTCCCCGCTG 637
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National Institutes of Health, M
Unpublished (1999)
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CN526117
CN526117.1 GI:46853770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
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Tissue Procurement: Dr. James Lin University of lowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                     GTGCTCCAGCTG
                                                                                                      TTCCTACCACATCCACTGCCTGAACCCCCCCCCCGCTGCCAGAGATCCCANACGGCGAATGGCT
                                                                                                                                                                                                                                                  GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HN0"
/clone_lib="NIH_BMAP_HN0"
/note="Torgan: Head; Vector: pYX-Asc; Site_1: EcoR I;
/note="Torgan: Head; Vector: pYX-Asc; Site_1: EcoR I;
/site_2: Not_I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not_I site. Double strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                       primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXY-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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Pred. No. 0.0028;
0; Mismatches 4
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RESULT 54
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.
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CB523529
GB0 bp mRNA linear EST 09-JUL-U1-M-GH0-cer-1-07-0-U1.rl NIH BMAP_GH0 Mus musculus cDNA clone IMAGE:6843512 5', mRNA sequence.
CB523529
CB523529 1 GI:29356884
EST.
Mus musculus (house mouse)
Mus musculus
   BU056500
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                                                                                                                                                              CTGTCCCCGCTG 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="phi08 (T1 phage resistant)"
/clone_lib="NIH BMAP_GHO"
/clone_lib="NIH BMAP_GHO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector. The library tag
Bequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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Pred. No. 0.0028;
0; Mismatches 4
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   mRNA
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EST 26-AUG-2002
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                          RESULT 55
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Io
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Io
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 751)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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                                                                                                                                                              CIGICCCCGCIG 499
                                                                                                                                                                                                                                                                                                                                                                                                                    GGAATTCTGTCGCGTCTGCAAGGACGGCGGNGAGCTCCTGTGCTGACACATGCCCTTC 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="embryo 12 Sapc"
//dev stage="embryo 12 Sapc"
//lab host="DH10B (T1 phage resistant)"
//clome lib="NIH_BMAP FOO"
//clome lib="NIH_BMAP lib="NIH-BMAP lib=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="whole brain"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="IMAGE: 6409023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62.2; DB 5; Pred. No. 0.0028;
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776
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DNA
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linear
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University of Iowa
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Mus musculus molossinus Mus musculus molossinus
                                                                                                                                                                                                                                                                                                                              791 GGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                          731 GGAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGGAGGAGGAGGTAAGAGGTCCACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector
R.Site 1
R.Site 2
 tigr-gss-dog-17000326704476 Dog Library Canis familiaris genomic, genomic survey sequence.
CE173623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, J. (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9110, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hattori,M., Toyoda,A., Noguchi,H., BAC end Sequences of Library MSMg01 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing : TJ
LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
                                                                                                                                                                                  TGAGGGTCAGC 921
                                                                                                                                                                                                                                                        TGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACCCCCTACTGTGTGGGTCC
                                                                                                                                                                                                                                                                                            GGAGCCCAAAGCCAGCTCTGATGCTGTCACATATGTGAACCTGCTGGCCCCACACCC
                                                                                                                                                                                                                                                                                                                                                                  GGAATTCCAGATCCTCGTGGGACTGAGGTCAGCTTCAGAGAAAACCAGGGGCCCCGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub species="molossinus"
/sub_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone="MSMG01-481F17.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="male"
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Pred. No. 0.0035;
0; Mismatches 6
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                                                      GSS 25-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 GGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kirkness EF
The Institute for Genomic
Department of Eukaryotic G
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 434) Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, Quackenbush, J. and Keele, J.W. Porcine gene discovery by normalized cDNA-library se EST cluster assembly Mamm. Genome 13 (8), 475-478 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 262)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                            434
141780 MARC 1PIG Sus scrofa c
BE234617
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                                                         Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                      2226715
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/note="Site 1: BstXI; Libraries
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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Pred. No. 0.0034;
0; Mismatches 4
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RESULT 58
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                                                                                                                                                      1 (bases 1 to 670)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed sembryos representing early developmental stages (2003)
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        670
885797 MARC 4PIG Sus scrofa c
CF792818
CF792818.1 GI:37797379
EST.
cross_match v0.990329.
Plate: TMW8013 row: I column: 11
Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 79 row: P column: 20
Seq primer: ATTTAGGTGACACTATAG
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Single pass sequencing. Bases called and alt trimmed with phred
v0.989904.e. Vector identified by cross_match with the -minscore 18
                                                        Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and -minmatch 12 options. PCR PRimers
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGATTTGCACTTTCTGCCGAGACTTATCCAAACCAGAAGTTGAGTATGATTGTGATGCT
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_llb="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2:
Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
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/mol_type="mRNA"
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Pred. No. 0.004;
0; Mismatches
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RESULT 59
CF794185
LOCUS
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ACCESSION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 672)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed sembryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672 bp mRNA linear
889669 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
CF794185
CF794185.1 GI:3779874A
                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
cross match v0.990329.
Plate: TMW8013 row: I column: 11
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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Sum scrofa (pig)
Sum scrofa
                                                                                                                                                                                                                                                                                                                                                        Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
/clone_lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary made with combined RNA from day-10, day-13,
fay-15, day-25, and day-30 whole embryos."
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/note="Vector: pcDNA3.; Site_1: EcoRI; Site_2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                              /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                   1. .672
                                                                                                                                                                           organism="Sus scrofa"
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/mol_type="mRNA"
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/lab_host="DH10B"
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Pred. No. 0.0042;
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Sus.
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Best Local Similarity
                                                                                                                                                                      Matches 110;
                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                          528 AATGAGGACGAGTGTGCCGTGTGTCGGGACGCGGGGGAGCTCATCTGCTGTGACGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 402 762 4550
Email: smitheemail.marc.usda.gov
Cincle bass sequencing. Bases called with phred v0.020425.c and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith,T.P.L., Fraking,B.A., Ford,J.J., Vallet,J.L., Nonneman,D.J., Wray,J.E. and Keele,J.W. Porcine EST collection using a normalized library coembryos representing early developmental stages Unpublished (2003)
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Plate: TMW8048 row: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCAGTCACAA 234
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  CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACC 647
                                                      AATGAGGACTGGTGTGTGTGTCAGAACGGGAGGGGAACTCCTGTGCTGTGAGAAGTGT
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primer: TAGAAGGCACAGTCGAGG.
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                    /clone_lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not
/inbteary made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                             Score 61.4; DB 7
Pred. No. 0.0043;
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Pred. No. 0.0042;
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Sus.
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Unpublished (1999)

Contact: S.L. Johnson
Washington University School of Medicine
Washington University School of Medicine
1314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810
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159a10.x1 Sugano Kawakami zebrafish DRA Danio rerio CDNA clor INAGE:3818011 3' similar to SW:CHD4 HUMAN Q14839 CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consortium/LLNL, send emai 
Seq primer: T7 from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 520)
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio (zebrafish)
Danio rerio
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                                                                                                    / CLUBE - INVADE - STANDARY CONTROL OF STANDAR
                                                               sequencing: 5' end primer coaccTGCAGCTCGAGCACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="AB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:3818011"
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     Score 61;
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REFERENCE
AUTHORS
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Email: genome-res@gc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
                                                                                                                                                                                                  1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BY389139
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 ATCCACTGCACCCCCCCCCCCGCTGCCAAAGATCCCAAAGGGCGAATGGCTCTGTCCCCGC
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                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 804)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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UI-M-HS0-cqi-o-05-0-UI.rl NIH_BMAP_HS0 Mus musculus cDNA clone
IMAGE:30674548 5', mRNA sequence.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                         clone was contributed by the Brain Molecular Anatomy Project
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/strain="C57BL/6J"
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/dev_stage="blastocyst"
/clone_lib="RIKEN full-length enriched, blastocyst"
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EST 29-APR-2004

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Query Match
Best Local
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutvyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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AL066051.1 GI:4945019
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope.
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/clone lib="NIH BMAP HS0"
/clone lib="NIH BMAP HS0"
/note="Organ: Upper Head; Vector: pYX-Asc; Site_1: EcoR I;
/note="Cryan: Upper Head; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site_Double strand cDNA was
size selected according to mRNA size fraction, ligated
size selected according to mRNA size fraction, ligated
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/mol_type="mRNA"
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/dev_stage="embryo 9.5 - 10.5 dpc"
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segref@genoscope.cns.fr
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RESULT 64 CNS006XK/c

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1 (bases 1 to 359)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                     359 bp
QV4-BN0090-020600-236-g06 BN0090
                Brazi
                               Rua Prof. Antonio
                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                  Contact: Simpson A.J.G.
                                                                                                                                      Proc. Natl.
                                                                                                                                                       sequence tags
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/db_xref="taxon:7227"
/clone="BACR14N09"
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/note="end : T7"
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                                                                                                                                                    Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/humanfl.html
Seq primer: pYX-5.
                                                                                                                                                                                                                        Coordinated Laboratory for Computational Genomics University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 bp UI-HF-BNO-ank-f-11-0-UI.r1 NIH NIH NAGE:3093236 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                      discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 461)
Bonaldo, M.F., Lenno
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CF137810.1 GI:33253254
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Seq primer: puc 18 forward
High quality sequence stop: 359.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-BN0090-020
                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                      Tissue Procurement: Louis Staudt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
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ORGANISM
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El (bases 1 to 544)

El NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UI-HF-BNO-aek-f-09-0-UI.r2 NIH MGC 50 Homo sapiens IMAGE:3064481 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                  Seq primer: M13 Forward
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llarity 61.5%;
Conservative
/tissue_type="lymph"
/cell_type="germinal center
/cell_line="MGCBS"
/lab_host="DH10B (LTI)"
/clone_lib="NHH_MGC_50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 50"
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/constructed_from_size_fractionated_cytoplasmIc_mRNA
(3.5-4.4kb). Directionally_cloned. Cells_provided_by
Louis_M. Staudt, Ph.D. Library_preparation_by_Maria_de
Fatima_Bonaldo, Ph.D. and M. Bento_Soares, Ph.D. "
                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:3064481"
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                                                                                                                                                    organism="Homo sapiens"
|mol_type="mRNA"
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/db_xref="taxon:9606"
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Pred. No. 0.0084;
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hw37c03.y1 Human primary human
Homo sapiens cDNA clone hw37c03
CN483764 GI:46565268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: graeme@helix.nih.gov
Plate: 37 row: c column: 03
Seq primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Section on Molecular Structure
National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsai, J.Y. and Wistow, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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/note="Organ: Eye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGATCGCGAGCGGCCCCT[715-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH, Bethesda, MD
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                                                                                                                                                                                                                                                                  /clone lib="Human primary human ocular pericytes.
Unamplīfied (hw)"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw37c03"
                                                                                                                                                                                                                                                                                                                               dev_stage="Adult"
                                                                                                                                                                                                                                                                                                           lab_host="EMDH10B"
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                                                                            532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                           Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1532-3 Yana, Kisarazu,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 683)
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ilarity 61.5%;
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/note="Vector: pME18SFL3; mRNA from
cells after 2-weeks retinoic acid (F
                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2001829"
                                                          TTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                  /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
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         BE258675 700 bp mRNA linear EST 13-JUL-20
6011116344F1 NIH MGC_16 Homo sapiens cDNA clone IMAGE:3356962 5',
mRNA sequence.
BE258675
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1 (Dases 1 to 699)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_16"
/clone_tib="NIH_MGC_16"
/clone_Torgan: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcorI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.0088;
0; Mismatches 60; Indels
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 731)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                     BE176589
RC3-HT0585-010400-023-c04
BE176589
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="pH10B (phage-resistant)"
/clone lib="NH10B (phage-resistant)"
/clone lib="NIH_MGC 16"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/cored into EcoRI/XhoI sites using the following 5;
/cloned into EcoRI/XhoI sites using the following 4;
/cloned into EcoRI/XhoI sites using the following 4;
/cloned into EcoRI/XhoI sites using the following 4;
/cloned into EcoRI/XhoI sites using the following 5;
/cloned into EcoRI/XhoI sites using 
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3356962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="retinoblastoma"
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HT0585 Homo sapiens cDNA,
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COMMENT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=RC3-HT0585-010400-023-c04&t3=2000-04-01&t4=1)
                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 750)
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Ludwig Institute for Cancer Research
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                                                                  Unpublished (1999
                                                                                                                                                                                            Homo sapiens (human)
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/note="Organ: head neck; Vector: puc18; Site_1: Smal;
/note="Organ: head neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="HT0585"
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Preparation: Ling Hong/Rubin Laboratory
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Pred. No. 0.0089;
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652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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BE259148
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Incyte Genomics, Inc. Characteristic Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_susing the
Directionally_cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                         LLCM130 row: e column:
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3344251"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.0089;
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  Query Match
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N AGENCOURT 7892893 NIH_MGC 72 H;
5', mRNA sequence.
BQ437443
BQ437443.1 GI:21176519
EST.
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                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13503 row: e column: 14
High quality sequence stop: 649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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/clone lib="NH10B (phage resistant)"
/clone lib="NH MGC 16"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                      /organism="Homo sapiens"
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/clone="IMAGE:6157429"
/tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
                                                          /clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo a Average insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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  3.9%;
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                                                                                                                     532 AGGACGAGTGTGCCGTGTGTCGGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                                           592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACCTGGA 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 AGGACGAGTGTGCCGTGTGTCGGGGAGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
64
                                                                                                                                                                                    96;
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1 (bases 1 to 948)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (LTNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium/LLNL at: image.llnl.gov found through the I.M.G.E. Consortium/LLNL at: image.llnl.gov Plates: LLCM54 row: C column: 23 High quality sequence stop: 746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600944490F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960590 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                        AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
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                                                                                                                                                                                                                                                                                      /clone="IMAGE:2960590"
/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 17"
/clone_lib="NIH MGC 17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally_cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
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|mol_type="mRNA"
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Pred. No. 0.0091;
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Euteleostomi;

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RESULT 78
BM457082
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Matches 96
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989 bp
AGENCOURT 6406806 NIH MGC 92 Homo
5', mRNA sequence.
BM457082
                                                                                                                                                                                                                                                                                                                                                                                                                           96;
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1 (bases 1 to 974)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG394104.1 GI:13287552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999
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                                                                                                                                                                                                                                                                                           GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 159
                                                                                                                                                                      GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:4579048"
/tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_16"
/clone_lib="NIH_MGC_16"
/clone="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/coned into EccRI/XhoI sites using the following 5'
adaptor: GCCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Robin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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sapiens cDNA clone
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s cDNA clone IMAGE:4579048 5',
                                           EST 05-FEB-2002
MAGE:5583326
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SOURCE
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Best Local S
Matches 96
                                                                JOURNAL
                                                                                                                                                                                          ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                              158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
                                                          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1011)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12346 row: d column: 15
                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                        BF309509.1
                                                                                                                                                                                                                                                                                                                   601892016F1 NIH_MGC_17 Homo
                                                                                                                                                                                                                                                                                                                                         BF309509
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Location/Qualifiers
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                               mRNA sequence.
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larity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryonal carcinoma, cell line"
/lab host="PH108 (phage-resistant)"
/clone_lib="NIH_MGC_92"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; Oilgo-dT primed.
Average insert size_2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5583326"
                                                                                                                                                                                                                                                        GI:11256902
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Indels

0;

Gaps

157 651 97 591 0

linear

Euteleostomi; Homo.

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RESULT 80
BQ213031
LOCUS
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Best Local Similarity
Matches 96; Conserv
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source
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BQ213031
BQ213031.1 GI:20393828
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAN13346 row: h column: 04
High quality sequence stop: 446.
                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 1365)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4137843"
/cissue_type="rhabdomyosarcoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.0092;
0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOllveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-EN0063-301000-001-e05&t3=2000-10-30&t4=1)
Seg primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laborzatory of Cancer Ceenetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
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BF847408
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                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
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                                                                                                                      quality sequence stop:
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGB:6067251"
/tissue_type="embryonal carcinoma, cell line"
/lab host="bH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/clone="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                            Location/Qualifiers
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Pred. No.
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EN0063 Homo sapiens cDNA,
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Query Match
Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
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Best Local Similarity
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AGENCOURT 7840454 NIH MGC 67
5', mRNA sequence.
BUI93516
                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13474 row: k column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 885)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                       Similarity
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    Conservative
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                                                                                                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/clone_lib="EN0063"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:6146430"
                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
|mol_type="mRNA"
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                    3.9%;
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Score 59.8; DB Pred. No. 0.01; 0; Mismatches
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Pred. No. 0.0093;
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    72;
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                                       Length 885;
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  Gaps
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BU527069
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1 (bases 1 to 918)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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AGENCOURT 10155962 NIH MGC 101 Homo
IMAGE:6536820 5', mRNA sequence.
BU527069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2698 row: m column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                     Similarity
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GGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                  /tissue_type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_101"
/clome_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
/note="Organ: lung; Vector: pOTB7; Directtionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:6536820"
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sapiens cDNA clone
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RESULT 85
BQ722521/c
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ORGANISM
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Matches 103; Conserv
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BQ722521 1104 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8219490 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6188186 5', mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2703 row: c column: 08

High quality sequence stop: 683.

Location/Qualifiers
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1 (Dases 1 to 943)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT 10182979 NIH MGC 101 Homo
IMAGE:6538496 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone lib="MIH_MGC_101"
/clone lib="MIH_MGC_101"
/note="Organ: lung; "Vector: pOTB7; Site_1: EcoRI; Site_2:
/note="CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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Pred. No. 0.01
0; Mismatches
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Best Local Similarity
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                                                                  1012 GCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCT 1071
                                                                                                                                                        952 TGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGC
                                                                                                                                                                                                       732 GÉCGGÉCECGGGÉCEGGÉCÉCCECNECECGGCÉCGÉCECECGGGÉCECGGGGÉGGÉCE
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                                                                                                                                                                                                                                                                                                  832 ACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                     772 AGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC
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1 (bases 1 to 1104)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Plate: LLAM13583 row: g column: 03
High quality sequence stop: 297.
Location/Qualifiers
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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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BQ722521.1 GI:21861418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected:
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylo
College of Medicine); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCrW-SPORT6 (Life Technologies); Sit
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="IMAGE:6188186"
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/mol_type="mRNA"

/db_xref="taxon:9606"
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Pred. No. 0.013;
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BQ672163
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Best Local S
Matches 276
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                                                                         276;
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AGENCOURT_8302070 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6274983
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ672163
BQ672163.1 GI:21782997
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Plate: LLCM2457 row:
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                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
ATGAGAGAGTGCTGAGAAGGACACCTCCTTCCTCAGTCCTGGAAGC 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCCGTCCGGCGGCCCCTCCCTCCTGACCCCAGATGGCCGGGACATGCAGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 306.
                                                                         Conservative
                                                                                                                                                                           /Clone="IMACS:6274983"
/clone="IMACS:6274983"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcORI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /moi_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
|mol_type="mRNA"
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                                                                                          3.8%;
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                                                               Score 58.8; Db 5;
Pred. No. 0.017;
""matches 592;
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                                                                                                                Length 1132;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1350)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                             1350
AGENCOURT_6393396 NIH_MGC_72
5', mRNA sequence
                                                                                                                                                                                            5', mRNA sequence.
BM450237
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                                                                                                                     Homo sapiens
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                                                                           Euteleostomi;
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MAGE:5528315
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Contact: Robert Strausberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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          NNCNCCCCCCCCNNGNCCCCCCGCGCGCGCGCGCGCCNNCCCNCGNGCCGGNGCCCGC
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                                         CACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGA
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llarity 41.0%;
Conservative
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_72"
/clone="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo c
Average insert size 2 kb. Library constructed by Life
Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.02;
0; Mismatches 378;
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                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                      CNS0072Q 932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                       fly), genomic survey sequence. AL066742 AL066742.1 GI:4945205
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB606244 416 bp mRNA line AMGNNUC:SRPB2-00055-Cl1-A srpb2 (10220) Rattus clone srpb2-00055-cl1 5', mRNA sequence.
      Genoscope.
Direct Submission
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Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
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                                       (bases 1 to 932)
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/mol type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2-00055-c11"
/tissue_type="prostate_tissue"
/clone_Tib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; rat
prostate normalized double selected poly(A+) mRNA size
fraction > 1 kb"
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Pred. No. 0.01
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 302)
Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H., Takeda, J., Ohara, O. and Seino, S.
                                                                                                                                                                                                                                                                      BP761124 302 bp mRNA BP761124 mouse (C57BL/6) pancreatic isle recombination-based method Mus musculus
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                                                                                                                        Mus musculus
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BP761124
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CSCSMSCCCCGCASCVCAGCCMSAGCMGCGCCMCCCGCCASCGSCCSCCCY 510
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                                                                                                                                                  musculus (house mouse)
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ilarity 31.0%;
Conservative 8
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/db_xref="taxon:7227"
/clone=BacR14B09"
/clone lib="RPCI-98"
/note="end: T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Drosophila melanogaster"
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Pred. No. 0.021
81; Mismatches
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AUTHORS
TITLE
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ORGANISM
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 bp
UI-M-GH0-cha-c-05-0-UI.rl NIH_BMAP_
IMAGE:30533716 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray Unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                         sequence: 302-357, > (GGA) n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 357)
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Fax: 81-78-382-5370
                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                        following repetitive elements were found
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/clone lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"
                                                  Location/Qualifiers
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mic01051"
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       /organism="Mus musculus"
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102;
                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefi.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF535776 361 bp
UI-M-GHO-cha-c-15-0-UI.r1 NIH BMAP
IMAGE:30533726 5', mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 361)
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CF535776.1 GI:34587744
                                           sequence: 302-359, >(GGA)n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                         following repetitive elements were found in this cDNA
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llarity 58.3%;
Conservative
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/dev_stage="1, 5, and 15 days newborn"
/lab_nost="whole try phage resistant)"
/clone_lib="NIH_BMAP_GHO"
/clone_lib="NIH_BMAP_GHO"
/note="forgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/clone="Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                       Location/Qualifiers
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30533716"
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Pred. No. 0.021;
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Matches

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REFERENCE AUTHORS TITLE

COMMENT

FEATURES

RESULT 92 CF535776 LOCUS

DEFINITION

ACCESSION VERSION

KEYWORDS

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AUTHORS
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 GTGCCTACCACCTCGTCTGCCTTGACCCCGAGCTTGACCGGGCTCCTGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 428)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project
                                                                                              Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Ld Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA839768 428 bp mRNA linear EST 27-FEB-1998 vw51dll.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone tmAGE:1247349 5' similar to TR:Q12873 Q12873 MI-2 AUTOANTIGEN 240
                                                                                                                                                                                                                                                                           Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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/dev stage="1, 5, and 15 days newborn"
/lab_nost="DH108 (T1 phage resistant)"
/clone lib="NIH BMAP GH0"
/clone lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP); 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   program coordinator.
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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58.3%;
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                                                                                                                                                          St. Louis,
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RESULT 94
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ORGANISM
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TITLE
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                              JOURNAL
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UI-M-GIO-cej-1-03-0-UI.r1 NIH BI
IMAGE:6840436 5', mRNA sequence
CB520637

CB520637.1 GI:29353992
EST
EST
Mus musculus (house mouse)

Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:661037
sequence: 385-450, >(GGA)n#Simple_repeat
          (BMAP)
The following repetitive elements were found
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCCTTCCACCTGGCCTGTCCCTGTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
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quality sequence stop: 419.
   Location/Qualifiers
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                                                    clone was contributed by the Brain Molecular Anatomy Project
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="mammary gland"
/dev_stage="4 weeks"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 0.02:
0; Mismatches
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AUTHORS
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CF911441
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MEDLINE
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Best Local
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, L
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0615 row: D column: 04
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 575)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript method cDNA librar:
                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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CF911441.1
                                                                                                           Contact: Dawood B. Dudekula
                                                                                                                                11544199
                                                                                                                                                       21429098
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                                                                                                                                                                                                                     submicrogram amounts of total RNAs by
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGB:6840436"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_tib="NH_BMAP_GIO"
/note="Organ: Brain, Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated at a agarose gel. First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site .Double strand cDNA was size selected according to mRNA size fraction, ligated with pools.
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/strain="C57BL/6"
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Cell (Lin-/c-Kit-/Sca-1+)
clone NIA:A0615D04
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BU703948
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTTGACGGCTGCCCTC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 690)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                          IMAGE:6406263 5', mRNA 6
BU703948
BU703948.1 GI:23631529
EST.
                                                                                                                                                                                                                                                                                                                                     BU703948
690 bp mRNA linear EST 15-JUL-2003
UI-M-FOO-bzr-e-16-0-UI.rl NIH_BMAP_FOO Mus musculus cDNA clone
IMAGE:6406263 5', mRNA sequence.
                                                                                                                                                                    Mus musculus
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High quality sequence stop: 575
                                                                                                                                                                                                       Mus musculus (house mouse)
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Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). (PMID: 11544199]). Total
RNAs were obtained from Drs. Dennis Taub, Dan Longo
(National Institute on Aging, USA), Jonathan Keller
(National Cancer Institute, USA), Jonathan Keller
(DAS were amplified by purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by Dhenol/chloroform and Centricon
100. The cDNAs were digested with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.2 kb. The library was
constructed by Yulan Plao."
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/mol_type="mRNA"
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/clone="NIA:A0615D04 IMAGE:30749031"
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|db_xref="niaEST:A0615D04-5"
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58.3%;
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                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                   Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230201M16 product:Mi-2 autoantigen 240 kDa protein (fragment) homolog [Homo sapiens], full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Mus musculus (house mouse)
                                                                                                          AK045449
                                                                                                                                                                                                                                          AK045449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   > (GGA) n#Simple repeat
Seq primer: pYX-5.
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                                                  HTC; CAP trapper.
                                                                           AK045449.1 GI:26337378
                                                                                                                                insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following repetitive elements were found in this cDNA equence: 1-42, >(CAG)n#Simple_repeat 647-690,
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                                                                                                                                                                                                                                                                                                                                                                          GCTGCCCCCACTGTGAGAAGGAGGGGGGGTGCAGTGGGAGGAGGAGGAGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_host=="DH10B (TI phage resistant)"
/clone lib="NIH BMAP FOO"
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pXX- Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according
SonalMo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
lowa Brain Anatomy Project (BMAP); 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6"
/db_xref="taxon:10090"
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Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Functional annotation of a full-length
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                               URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details
                                                                                                                                                                                                                                                                                                                                                Division of Experimental Animal Research
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/organism="Mus musculus"
/mol_type="mRNA"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 AGGACGAGTGTGCCGTGTGTCCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequenc BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefægenoscope.cr - Web : www.genoscope.crs.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Eukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence T7 end of EBACR14B09 of RPCI-98 library from Drosophila melanogaster
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AL066742
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GSEYGTGPGRKRARKHRGPKKQKENKPGKPKRKKKLDSEBEPGSERDEYREKSESG
GSEYGTGPGRKRARKHREKKEKKTKRRKGEGDGGHKQVEQKSATILLTWGLEDVEH
VPSEDYHTLTNYKAFSGPMRPLI AKKONFKI EN KMWTILIGAKWRETSANNPEKGSA
AVAAAAAAAAAAVAEQVSAAVSSATPIAPSGPPPALPPPAPEIQPPIRRAKTKEGK
GPGHKRINKSPRVPDGRKKLRGKWAPLKI KLGLLGGKRKAGSCAFQSEEGHEPEAP
ESDLDGGSVHSASGWPDGPVRAKKLKGKFPGRKKKKVLGFAVTGEBEVDGYETDHQD
YCEVCQQGGEIIILCDTCPRAYHLVCLDPELDRAPEGKWSCPHCEKEGVQWEAKKEEEE
ESDLDSGSVHSASGWPDGPVRAKKLKGRFPGRKKKKVLGPAVTGEBEVDGYETDHQD
YCEVCQQGGEIIILCDTCPRAYHLVCLDPELDRAPEGKWSCPHCEKEGVQWEAKKEEEE
ESDEBGEKEEEDDHWEYCRVCXDGGELLCCDACISSYHHCLWPPLPDIPRGEWLC
PRCTCPVLKGRVQKILHWRWGEPPVAVVPAPQADAGNPDVPDRCDGRSEREFFVKWV
GLSYWHCSWAKEIQLEIITHLVWYRNYQKKNDWDEPPDLOGRSEREFFVKMV
TAPMERGYYRFGIKPEWMTVHRIIINHADKKGNYHYLVKWKDLPYDQSTWEEDEMNIP
YAPMERGYYRFGIKPEWMTVHRIIINHADKKGNYHYLVKWKDLPYDQSTWEEDEMNIP
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evidence: FASTY, 9
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/db_xref="FANTOM_DB:B230201M16"
/db_xref="taxon:10090"
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129. .>2252
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/,
                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes DNA, cl.
AG057392
AG057392.1 GI:16594851
GSS.
                                                                                                                                                                                                                                                                                                                                                             Pan
                                                                                                                                                                                                                   BAC end sequences of Library PTB
                                                                                                                                                                                                                                        Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/mol type="genomic DNA"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14809"
/clone="BACR14809"
/clone_lib="RPCI-98"
/note="end : T7"
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nd Sakaki,Y.
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                                                                            BQ953925 1038 bp mRNA 1AGENCOURT_8803230 Lupski_sciatic_nerve Homo IMAGE:6198951 5', mRNA sequence.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC was generated during the R&D process and may have higher chance clone tracking errors.
                                                     BQ953925.1
                                                                 BQ953925
                            Homo sapiens (human)
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R.Site 1 : SacI
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Location/Qualifiers
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"
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                                                     GI:22369403
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLM
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: g column: 16
High quality sequence stop: 214.
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Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CCCGGCCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGAG
                                                                          CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sir
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGGGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Technologies."
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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Search completed: February 9, 2005, 17:40:05 Job time : 4565 secs 밁

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